

GenCore version 5.1.1.8
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OM protein - protein search, using sw model
Run on: May 15, 2006, 13:26:41 ; Search time 190 Seconds
(without alignments)
2594.647 Million cell updates/sec
Title: US-10-602-441-4
Perfect score: 5901
Sequence: 1 MTRAPRCFAVRSLLRSRYRE.....TILKAADPALSTDFQTILD 1122
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5901	100.0	1122	2	AAY26579 Murine te
2	5901	100.0	1122	8	ADG90601 Murine TE
3	5954	99.2	1122	5	ABR06711 Mouse tel
4	4859	82.3	1122	8	ADG90609 TERT cons
5	4751	80.5	1128	7	ADD21416 Golden ha
6	4751	80.5	1128	8	ADG90603 Hamster T
7	3505	59.4	1132	2	AAY46957 Human tel
8	3505	59.4	1132	2	AAY90251 Human cat
9	3505	59.4	1132	2	AAY28881 Human tel
10	3505	59.4	1132	2	AAY32090 Human tel
11	3505	59.4	1132	2	AAY43621 A human t
12	3505	59.4	1132	2	AAY26580 Human tel
13	3505	59.4	1132	4	AAG64859 Heart mus
14	3505	59.4	1132	4	AAG64329 Human pro
15	3505	59.4	1132	4	AAB99930 Human tel
16	3505	59.4	1132	4	AAB82765 Human tel
17	3505	59.4	1132	5	AAB29226 Human tel
18	3505	59.4	1132	5	AAY72735 Human tel
19	3505	59.4	1132	6	ABR42384 Human tel
20	3505	59.4	1132	6	ABR42063 Human tel
21	3505	59.4	1132	6	ABP56676 Human tel
22	3505	59.4	1132	6	ABR58045 Human tel
23	3505	59.4	1132	7	ADD21420 Human TER
24	3505	59.4	1132	7	ADH72743 Human pro

25	3505	59.4	1132	8	ADG70114	Adg70114 hTERT pro
26	3505	59.4	1132	8	ADG90599	Adg90599 Human TER
27	3505	59.4	1132	8	ADI82172	Adi82172 Human tel
28	3505	59.4	1132	8	ADR70482	Adr70482 Human tel
29	3505	59.4	1132	9	ADY25759	Ady25759 Human tel
30	3505	59.4	1154	2	AAW61350	AAW61350 Human tel
31	3505	59.4	1189	2	AAW47008	AAW47008 Glutathio
32	3498	59.3	1285	2	AAW47000	AAW47000 HIS tagge
33	3498	59.3	1132	2	AAW71376	AAW71376 Human tel
34	3498	59.3	1132	2	AAY00627	Aay00627 Human tel
35	3498	59.3	1132	2	AAY00638	Aay00638 Truncated
36	3498	59.3	1132	2	AAY28401	Aay28401 Human EST
37	3498	59.3	1132	3	AAY96566	Aay96566 hEST2, a
38	3498	59.3	1132	7	ADC47061	Adc47061 Human TER
39	3498	59.3	1132	7	ADA40482	Ade40482 Human tel
40	3498	59.3	1132	9	AEA38666	Aea38666 Human tel
41	3496	59.2	1132	2	AAW56113	AAW56113 Human tel
42	3486.5	59.1	1199	2	AAW47007	AAW47007 Glutathio
43	3471	58.8	1166	2	AAY00647	Aay00647 Telomeras
44	3463	58.7	1405	2	AAW56101	AAW56101 Enhanced
45	3435	58.2	1120	2	AAW00641	AAW00641 Telomeras

ALIGNMENTS

RESULT 1
AAY26579
ID AAY26579 standard; protein; 1122 AA.
XX AC AAY26579;
XX DT 13-SEP-1999 (first entry)
XX DE Murine telomerase reverse transcriptase (mTERT) enzyme.
XX KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication.
XX OS Mus sp.
XX PN WO9927113-A1.
XX PD 03-JUN-1999.
XX PF 25-NOV-1998; 98WO-US025211.
XX PR 26-NOV-1997; 97US-00979742.
PR 16-MAR-1998; 98US-00042460.
XX (GERO-) GERON CORP.
XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX PI Morin GB, Allsopp R, Depinho R, Greenberg R;
XX WPI; 1999-347722/29.
XX N-PSDB; AAX80994.
XX Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
XX nucleic acids.
XX Claim 8; Fig 2; 135pp; English.
XX The invention relates to a mouse telomerase reverse transcriptase (mTERT)
XX enzyme. Compositions containing mTERT can be used in telomere length
XX assays. Isolated mTERT is useful as an immunogen for the production of
XX monoclonal or polyclonal antibodies. The method is useful for assessing
XX the degree of purification and identification of new mTERT species, such
XX as an mTERT allele, homolog or isoform, or to screen for modulators
XX (antagonists and agonists) of telomerase-mediated DNA replication.
XX Antagonists and agonists of mTERT can be used to modify the activity of
XX other telomerase enzymes such as human TERT (hTERT). The present sequence
XX represents a mTERT enzyme

XX	SQ	Sequence 1122 AA;										
		Query Match	100.0%;	Score 5901;	DB 2;	Length 1122;						
		Best Local Similarity	100.0%;	Pred. No. 0;								
		Matches 1122; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;			
Qy	1	MTRAPRCAPVRSLLRSRYREVWPLATFVRRLGPEGRLVQGD	60									
Db	1	MTRAPRCAPVRSLLRSRYREVWPLATFVRRLGPEGRLVQGD	60									
Qy	61	GSQPPADLSFQVSSLSKELVARVVQRLCERNERNVLA	120									
Db	61	GSQPPADLSFQVSSLSKELVARVVQRLCERNERNVLA	120									
Qy	121	SYLPNTVITLTVSGAMLLLSRVGDDLLVYLLAHACALYLLVPPSCAYQVCGSPLYQICA	180									
Db	121	SYLPNTVITLTVSGAMLLLSRVGDDLLVYLLAHACALYLLVPPSCAYQVCGSPLYQICA	180									
Qy	181	TTDIWPSVSASVYRTPRGVGRPTNLRFLOQIKSSSRQEQAPKPLALPSRGTGRHLSLTSTS	240									
Db	181	TTDIWPSVSASVYRTPRGVGRPTNLRFLOQIKSSSRQEQAPKPLALPSRGTGRHLSLTSTS	240									
Qy	241	VPSAKKACYPVPRVEEGPHROVLTPSGKSWPSPAPSPVPTAEKDLSSKGKVSDDL	300									
Db	241	VPSAKKACYPVPRVEEGPHROVLTPSGKSWPSPAPSPVPTAEKDLSSKGKVSDDL	300									
Qy	301	SGSVCKHKPSPSTLSPPRQNAFQLRPFPIETRHFLYSGDQGERLNPSFLLSNLQPNLT	360									
Db	301	SGSVCKHKPSPSTLSPPRQNAFQLRPFPIETRHFLYSGDQGERLNPSFLLSNLQPNLT	360									
Qy	361	GARRLVEIIFLAGSRPRTSGPLCRTHLSRRYQWQRPPLFQOLLVNHAEQYVRLRSHCRF	420									
Db	361	GARRLVEIIFLAGSRPRTSGPLCRTHLSRRYQWQRPPLFQOLLVNHAEQYVRLRSHCRF	420									
Qy	421	RTANQOVTALNTSPHLLMDLLRLHSSPWQVYGLRACLCKVVSASLWGTGRHNERFPFN	480									
Db	421	RTANQOVTALNTSPHLLMDLLRLHSSPWQVYGLRACLCKVVSASLWGTGRHNERFPFN	480									
Qy	481	LKKPFLSGYKGLSLQELMWMKVEDCHWLSSPGKDRVPAAEHLRERILATFLFWLMD	540									
Db	481	LKKPFLSGYKGLSLQELMWMKVEDCHWLSSPGKDRVPAAEHLRERILATFLFWLMD	540									
Qy	541	TYVQLLRSFPYITESTFKQRLFPYRKSVSKLSIGVROHLERVRLRELSQEVRRHQ	600									
Db	541	TYVQLLRSFPYITESTFKQRLFPYRKSVSKLSIGVROHLERVRLRELSQEVRRHQ	600									
Qy	601	DTWLAMPICRLRFIPKPNGLRPIVNMYSMGTALGRKQAOHFTQRLKTLFSLMNYERT	660									
Db	601	DTWLAMPICRLRFIPKPNGLRPIVNMYSMGTALGRKQAOHFTQRLKTLFSLMNYERT	660									
Qy	661	KHPHLMGSSVLGMNDIYRTWAFVLRVLRALDQTPRMYPVKADVTGAYDAIPQGLVEVVA	720									
Db	661	KHPHLMGSSVLGMNDIYRTWAFVLRVLRALDQTPRMYPVKADVTGAYDAIPQGLVEVVA	720									
Qy	721	NMIRHSESTYCIQYAVVRRDSQGVHKSFRQVTTLSDLQPYMCQFLKHLQDSASALR	780									
Db	721	NMIRHSESTYCIQYAVVRRDSQGVHKSFRQVTTLSDLQPYMCQFLKHLQDSASALR	780									
Qy	781	NSVWTEQSTSMNESSSLFDFLHLRHSVVKIGDRCTQCQIPQGSLSLTLLCSLCFG	840									
Db	781	NSVWTEQSTSMNESSSLFDFLHLRHSVVKIGDRCTQCQIPQGSLSLTLLCSLCFG	840									
Qy	841	DMENKLFARVQDGLLRFDVDFLLVTPHLDOAKTFLSTLVHGVPEYGCMLNLTQVYVF	900									
Db	841	DMENKLFARVQDGLLRFDVDFLLVTPHLDOAKTFLSTLVHGVPEYGCMLNLTQVYVF	900									
Qy	901	PVEPGLTGGAAVQVLPQAHCLPWCGLLDDTQTLFVFCDSYGAQTSIKTSLTFQSVFKAG	960									
Db	901	PVEPGLTGGAAVQVLPQAHCLPWCGLLDDTQTLFVFCDSYGAQTSIKTSLTFQSVFKAG	960									
Qy	961	KTMNRKLLSVLRKCHGLFLDLQVNSLQTVCIYKIFLLQAYRPHACVYQIQLPFDQVRK	1020									
Db	961	KTMNRKLLSVLRKCHGLFLDLQVNSLQTVCIYKIFLLQAYRPHACVYQIQLPFDQVRK	1020									
Qy	1021	NLTFPLGIISQASCCYAILKVKNPGMTLTKASGSPPEAAHWLCYQAFLLKLAHSHVIYK	1080									
Db	1021	NLTFPLGIISQASCCYAILKVKNPGMTLTKASGSPPEAAHWLCYQAFLLKLAHSHVIYK	1080									
Qy	1081	CLLGPLRTAOKLLCRKLPEATMTILKAAADPALSTDFQTILD	1122									
Db	1081	CLLGPLRTAOKLLCRKLPEATMTILKAAADPALSTDFQTILD	1122									
RESULT 2												
ADG90601												
ID	ADG90601 standard; protein; 1122 AA.											
XX												
AC	ADG90601;											
XX												
DT	25-MAR-2004 (first entry)											
XX												
DE	Murine TERT SEQ ID NO:4.											
XX												
KW	mouse; immune response; telomerase reverse transcriptase; TERT; cytostatic; immunostimulant; cancer; cytotoxic T cell response.											
XX												
OS	Mus sp.											
XX												
PN	WO2004002408-A2.											
XX												
PD	08-JAN-2004.											
XX												
PF	24-JUN-2003; 2003WO-US019844.											
XX												
PR	27-JUN-2002; 2002US-0393295P.											
XX												
PA	(GERO-) GERON CORP.											
XX												
PI	Majumdar A, Ferber IA, Frolkis M, Wang Z;											
XX												
DR	WPI; 2004-071946/07.											
XX												
DR	N-PSDB; ADG90600.											
XX												
PT	Eliciting an immune response in a mammal specific for its own telomerase reverse transcriptase (TERT), useful for treating or preventing cancer, comprises administering a composition containing TERT of another mammalian species.											
XX												
PS	Claim 10; SEQ ID NO 4; 44pp; English.											
XX												
CC	The invention relates to a novel method for eliciting an immune response in a mammalian subject that is specific for its own telomerase reverse transcriptase (TERT), comprising administering an immunogenic composition containing a protein with at least 20 consecutive amino acids of TERT of another mammalian species, or a nucleic acid encoding the protein. A composition of the invention has cytostatic, and immunostimulant activity. The protein or the nucleic acid encoding the protein is useful in the manufacture of a medicament for the treatment of cancer in a human or for eliciting a cytotoxic T cell response in a human.											
XX												
SQ	Sequence 1122 AA;											
Query Match		100.0%;	Score 5901;	DB 8;	Length 1122;							
Best Local Similarity		100.0%;	Pred. No. 0;									
Matches 1122; Conservative		0;	Mismatches	0;	Indels	0;	Gaps	0;				
Qy	1	MTRAPRCAPVRSLLRSRYREVWPLATFVRRLGPEGRLVQGD	60									
Db	1	MTRAPRCAPVRSLLRSRYREVWPLATFVRRLGPEGRLVQGD	60									
Qy	61	GSQPPADLSFQVSSLSKELVARVVQRLCERNERNVLA	120									
Db	61	GSQPPADLSFQVSSLSKELVARVVQRLCERNERNVLA	120									
Qy	121	SYLPNTVITLTVSGAMLLLSRVGDDLLVYLLAHACALYLLVPPSCAYQVCGSPLYQICA	180									
Db	121	SYLPNTVITLTVSGAMLLLSRVGDDLLVYLLAHACALYLLVPPSCAYQVCGSPLYQICA	180									
Qy	181	TTDIWPSVSASVYRTPRGVGRPTNLRFLOQIKSSSRQEQAPKPLALPSRGTGRHLSLTSTS	240									
Db	181	TTDIWPSVSASVYRTPRGVGRPTNLRFLOQIKSSSRQEQAPKPLALPSRGTGRHLSLTSTS	240									
Qy	241	VPSAKKACYPVPRVEEGPHROVLTPSGKSWPSPAPSPVPTAEKDLSSKGKVSDDL	300									
Db	241	VPSAKKACYPVPRVEEGPHROVLTPSGKSWPSPAPSPVPTAEKDLSSKGKVSDDL	300									
Qy	301	SGSVCKHKPSPSTLSPPRQNAFQLRPFPIETRHFLYSGDQGERLNPSFLLSNLQPNLT	360									
Db	301	SGSVCKHKPSPSTLSPPRQNAFQLRPFPIETRHFLYSGDQGERLNPSFLLSNLQPNLT	360									
Qy	361	GARRLVEIIFLAGSRPRTSGPLCRTHLSRRYQWQRPPLFQOLLVNHAEQYVRLRSHCRF	420									
Db	361	GARRLVEIIFLAGSRPRTSGPLCRTHLSRRYQWQRPPLFQOLLVNHAEQYVRLRSHCRF	420									
Qy	421	RTANQOVTALNTSPHLLMDLLRLHSSPWQVYGLRACLCKVVSASLWGTGRHNERFPFN	480									
Db	421	RTANQOVTALNTSPHLLMDLLRLHSSPWQVYGLRACLCKVVSASLWGTGRHNERFPFN	480									
Qy	481	LKKPFLSGYKGLSLQELMWMKVEDCHWLSSPGKDRVPAAEHLRERILATFLFWLMD	540									
Db	481	LKKPFLSGYKGLSLQELMWMKVEDCHWLSSPGKDRVPAAEHLRERILATFLFWLMD	540									
Qy	541	TYVQLLRSFPYITESTFKQRLFPYRKSVSKLSIGVROHLERVRLRELSQEVRRHQ	600									
Db	541	TYVQLLRSFPYITESTFKQRLFPYRKSVSKLSIGVROHLERVRLRELSQEVRRHQ	600									
Qy	601	DTWLAMPICRLRFIPKPNGLRPIVNMYSMGTALGRKQAOHFTQRLKTLFSLMNYERT	660									
Db	601	DTWLAMPICRLRFIPKPNGLRPIVNMYSMGTALGRKQAOHFTQRLKTLFSLMNYERT	660									
Qy	661	KHPHLMGSSVLGMNDIYRTWAFVLRVLRALDQTPRMYPVKADVTGAYDAIPQGLVEVVA	720									
Db	661	KHPHLMGSSVLGMNDIYRTWAFVLRVLRALDQTPRMYPVKADVTGAYDAIPQGLVEVVA	720									
Qy	721	NMIRHSESTYCIQYAVVRRDSQGVHKSFRQVTTLSDLQPYMCQFLKHLQDSASALR	780									
Db	721	NMIRHSESTYCIQYAVVRRDSQGVHKSFRQVTTLSDLQPYMCQFLKHLQDSASALR	780									
Qy	781	NSVWTEQSTSMNESSSLFDFLHLRHSVVKIGDRCTQCQIPQGSLSLTLLCSLCFG	840									
Db	781	NSVWTEQSTSMNESSSLFDFLHLRHSVVKIGDRCTQCQIPQGSLSLTLLCSLCFG	840									
Qy	841	DMENKLFARVQDGLLRFDVDFLLVTPHLDOAKTFLSTLVHGVPEYGCMLNLTQVYVF	900									
Db	841	DMENKLFARVQDGLLRFDVDFLLVTPHLDOAKTFLSTLVHGVPEYGCMLNLTQVYVF	900									
Qy	901	PVEPGLTGGAAVQVLPQAHCLPWCGLLDDTQTLFVFCDSYGAQTSIKTSLTFQSVFKAG	960									
Db	901	PVEPGLTGGAAVQVLPQAHCLPWCGLLDDTQTLFVFCDSYGAQTSIKTSLTFQSVFKAG	960									
Qy	961	KTMNRKLLSVLRKCHGLFLDLQVNSLQTVCIYKIFLLQAYRPHACVYQIQLPFDQVRK	1020									
Db	961	KTMNRKLLSVLRKCHGLFLDLQVNSLQTVCIYKIFLLQAYRPHACVYQIQLPFDQVRK	1020									

Db 121 SYLNTVITETLRVSGAWMLLSRVGDDLLVYLAHCAVLLVPPSCAYQVCGSPLYQICA 180
Qy 181 TTDIWPVSASVYRTPRGVGRNTNLRFLQOIKSSSRQEQAPKPLALPSRGTKKHLSTSTS 240
Db 181 TTDIWPVSASVYRTPRGVGRNTNLRFLQOIKSSSRQEQAPKPLALPSRGTKKHLSTSTS 240
Qy 241 VPSAKKARCYVPVRVEEGPHRQVLPPTSGKSWVPSPARSPEVPTAEKOLSSKGKVDLSL 300
Db 241 VPSAKKARCYVPVRVEEGPHRQVLPPTSGKSWVPSPARSPEVPTAEKOLSSKGKVDLSL 300
Qy 301 SGSVCKKHPSTSLSPRONAFQLRPFIEHFLYSRQDQERLNPFLSNLPNLT 360
Db 301 SGSVCKKHPSTSLSPRONAFQLRPFIEHFLYSRQDQERLNPFLSNLPNLT 360
Qy 361 GARRLVEIIFLGSRRPRTSGPLCRTHLSRRYQWRPLFOQLLVNHAECQYVRLLSHCRF 420
Db 361 GARRLVEIIFLGSRRPRTSGPLCRTHLSRRYQWRPLFOQLLVNHAECQYVRLLSHCRF 420
Qy 421 RTANQOQVTDALNTSPPHLMDLLRLHSSPMQVYGFRLACLCCKVVSASLWGTNRNRRFPKN 480
Db 421 RTANQOQVTDALNTSPPHLMDLLRLHSSPMQVYGFRLACLCCKVVSASLWGTNRNRRFPKN 480
Qy 481 LKXPIISLGKYGKLSQELMWKQVEDCHWLRSRSPGKDRVPAAEHRLRERILATFLWLMD 540
Db 481 LKXPIISLGKYGKLSQELMWKQVEDCHWLRSRSPGKDRVPAAEHRLRERILATFLWLMD 540
Qy 541 TVVQVLLRSFFYITESTFOKNRLEFFYRKSVMKLSQISGVQHLRVRRLRELSQEEVRHQ 600
Db 541 TVVQVLLRSFFYITESTFOKNRLEFFYRKSVMKLSQISGVQHLRVRRLRELSQEEVRHQ 600
Qy 601 DTWLAMPICRLRFIPKPNGLRPIVNMYSMGTALRRKQAQHFQRLKTLFSLMNYERT 660
Db 601 DTWLAMPICRLRFIPKPNGLRPIVNMYSMGTALRRKQAQHFQRLKTLFSLMNYERT 660
Qy 661 KHPHLMGSSVLGNDIYRTWRAFVLRVLRALDQTPRMVFKADVTGAYDAIPQKLVVEVA 720
Db 661 KHPHLMGSSVLGNDIYRTWRAFVLRVLRALDQTPRMVFKADVTGAYDAIPQKLVVEVA 720
Qy 721 NMIRHSESTYCIQYAVVVRDSDGQVHKSFRRQVTTLSLQPYMGQFLKHLQSDASALR 780
Db 721 NMIRHSESTYCIQYAVVVRDSDGQVHKSFRRQVTTLSLQPYMGQFLKHLQSDASALR 780
Qy 781 NSWIEQSIEMNESSSLDFFLHFLRHSVVKIGDRCTYTCQGIPOGSSLSLTLCSLCFG 840
Db 781 NSWIEQSIEMNESSSLDFFLHFLRHSVVKIGDRCTYTCQGIPOGSSLSLTLCSLCFG 840
Qy 841 DMENKLFARVQRDGLLRVDDFLVTPHLDQAKTFLSTLVHGVPEYGCMLNLTQVNF 900
Db 841 DMENKLFARVQRDGLLRVDDFLVTPHLDQAKTFLSTLVHGVPEYGCMLNLTQVNF 900
Qy 901 PVEPTLGGAAVQYLPALHCLFWCGLLDTOTLEVPDYSYGAQTSIKTSLTFQSVFKAG 960
Db 901 PVEPTLGGAAVQYLPALHCLFWCGLLDTOTLEVPDYSYGAQTSIKTSLTFQSVFKAG 960
Qy 961 KTRMKNLLSVLRKCHGLFLDQVNSLQVVCINIYKIFLQAYRFHACVQLPFPQVRK 1020
Db 961 KTRMKNLLSVLRKCHGLFLDQVNSLQVVCINIYKIFLQAYRFHACVQLPFPQVRK 1020
Qy 1021 NLTFFLIGIISQASCCYAILKVNPGMTLKASGSPPEAAHWLCYQAFLLKLAHSHVYK 1080
Db 1021 NLTFFLIGIISQASCCYAILKVNPGMTLKASGSPPEAAHWLCYQAFLLKLAHSHVYK 1080
Qy 1081 CLLGPLRTAQKLCRLKPLATNTILKAAADPALSTDFQITLD 1122
Db 1081 CLLGPLRTAQKLCRLKPLATNTILKAAADPALSTDFQITLD 1122

RESULT 3
ABB06711
ID ABB06711 standard; protein; 1122 AA.
XX
AC ABB06711;

XX 11-JUN-2002 (first entry)
XX Mouse telomerase protein sequence.
XX
KW Mouse; telomerase; promoter; telomerase catalyst subunit; TERT; mTERT;
XX enzyme; transgenic mouse; drug development; anticancer.
XX Mus sp.
XX JP2002000121-A.
XX 08-JAN-2002.
XX 23-JUN-2000; 2000JP-00190137.
XX 23-JUN-2000; 2000JP-00190137.
XX (RIKO-) ZH RIKOGAKU SHINKOKAI.
XX (KIRI) KIRIN BREWERY KK.
XX WPI; 2002-298279/34.
XX
XX A transgenic mouse comprising a DNA promoter region of mouse telomerase
XX catalyst subunit (TERT) is used for the development of drugs and
XX anticancer agents for regeneration of tissues and organs.
XX Disclosure; Fig 3; 13pp; Japanese.
XX
XX The present invention describes a transgenic mouse (I) comprising a DNA
XX construct having a DNA containing a promoter region of mouse telomerase
XX catalyst subunit (TERT) and a DNA containing a reporter gene connected
XX under the control of the promoter region. The transgenic mouse can be
XX used in the development of drugs and anticancer agents for regeneration
XX of tissues and organs. The present sequence represents the mouse
XX telomerase protein, which is given in the exemplification of the present
XX invention
XX
XX Sequence 1122 AA;
Query Match 99.2%; Score 5854; DB 5; Length 1122;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1115; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MTRAPRCVAVSLRSLRSRYREVWPLATFVRRLGPEGRRLVQPGDKPIYRTLVAQCLVCMHW 60
Db 1 MTRAPRCVAVSLRSLRSRYREVWPLATFVRRLGPEGRRLVQPGDKPIYRTLVAQCLVCMHW 60
Qy 61 GSQPPADLSFHQVSSSLKELVARVVQRLCERNERNVLAFGPELLNEARGGPPMAFTSVR 120
Db 61 GSQPPADLSFHQVSSSLKELVARVVQRLCERNERNVLAFGPELLNEARGGPPMAFTSVR 120
Qy 121 SYLNTVITETLRVSGAWMLLSRVGDDLLVYLAHCAVLLVPPSCAYQVCGSPLYQICA 180
Db 121 SYLNTVITETLRVSGAWMLLSRVGDDLLVYLAHCAVLLVPPSCAYQVCGSPLYQICA 180
Qy 181 TTDIWPVSASVYRTPRGVGRNTNLRFLQOIKSSSRQEQAPKPLALPSRGTKKHLSTSTS 240
Db 181 TTDIWPVSASVYRTPRGVGRNTNLRFLQOIKSSSRQEQAPKPLALPSRGTKKHLSTSTS 240
Qy 241 VPSAKKARCYVPVRVEEGPHRQVLPPTSGKSWVPSPARSPEVPTAEKOLSSKGKVDLSL 300
Db 241 VPSAKKARCYVPVRVEEGPHRQVLPPTSGKSWVPSPARSPEVPTAEKOLSSKGKVDLSL 300
Qy 301 SGSVCKKHPSTSLSPRONAFQLRPFIEHFLYSRQDQERLNPFLSNLPNLT 360
Db 301 SGSVCKKHPSTSLSPRONAFQLRPFIEHFLYSRQDQERLNPFLSNLPNLT 360
Qy 361 GARRLVEIIFLGSRRPRTSGPLCRTHLSRRYQWRPLFOQLLVNHAECQYVRLLSHCRF 420
Db 361 GARRLVEIIFLGSRRPRTSGPLCRTHLSRRYQWRPLFOQLLVNHAECQYVRLLSHCRF 420
Qy 421 RTANQOQVTDALNTSPPHLMDLLRLHSSPMQVYGFRLACLCCKVVSASLWGTNRNRRFPKN 480

Db 421 RTANQVTDALNTSPHLLMDLRLHSSPMQVYGFRLACLCKVVSASLWGRNHRFPFN 480
Qy 481 LKXFTSLGKYKLSLOELMWKVEDCHWLSSPGKDRVPAAEHRLRRIIATFLFWM 540
Db 481 LKXFTSLGKYKLSLOELMWKVEDCHWLSSPGKDRVPAAEHRLRRIIATFLFWM 540
Qy 541 TVVOLLRSFFVITESTQKRLPYRKSVKLSQSIGVROHLRRLRELSQEVRRHQ 600
Db 541 TVVOLLRSFFVITESTQKRLPYRKSVKLSQSIGVROHLRRLRELSQEVRRHQ 600
Qy 601 DTWLAMPICRLRFPKPNGLRPIVNMYSMGTGRALGRKQAHFTQRLKTLFSLMNTV 660
Db 601 DTWLAMPICRLRFPKPNGLRPIVNMYSMGTGRALGRKQAHFTQRLKTLFSLMNTV 660
Qy 661 KHPHLMGSSVLGMDNIYRTWAFVLRLVRLALDQTPRMVFKADVTDGAYDAIPQGLVEVVA 720
Db 661 KHPHLMGSSVLGMDNIYRTWAFVLRLVRLALDQTPRMVFKADVTDGAYDAIPQGLVEVVA 720
Qy 721 NMIRHSESTYCIROYAVVRDSQGVHKSFRQVTTLSDLQPMGQFLKHLQDSDASALR 780
Db 721 NMIRHSESTYCIROYAVVRDSQGVHKSFRQVTTLSDLQPMGQFLKHLQDSDASALR 780
Qy 781 NSVVEIQISWNSSSFLDFLHFLRHSVVKIGDRCYTQCQIPQGSLSLTLCSLCFG 840
Db 781 NSVVEIQISWNSSSFLDFLHFLRHSVVKIGDRCYTQCQIPQGSLSLTLCSLCFG 840
Qy 841 DMENKLPFAVQRDGLLLRFDVDFLLVTPHLDOAKTFLSTLVHGVEYGCMLNLOKTVNPF 900
Db 841 DMENKLPFAVQRDGLLLRFDVDFLLVTPHLDOAKTFLSTLVHGVEYGCMLNLOKTVNPF 900
Qy 901 PVEPTLGGAPYQOLPAHCLFPMCGLLDQTLVFCDSYGAOTSIKTSLTFOSVFKAG 960
Db 901 PVEPTLGGAPYQOLPAHCLFPMCGLLDQTLVFCDSYGAOTSIKTSLTFOSVFKAG 960
Qy 961 KTMNKLLSVLRKCHGLFDLQVNSLQTVCNINIKIFLLQAYRPHACVLIQLPDQVRK 1020
Db 961 KTMNKLLSVLRKCHGLFDLQVNSLQTVCNINIKIFLLQAYRPHACVLIQLPDQVRK 1020
Qy 1021 NLTPFLGIISQASCCYAILKVQNGMTLKASGFPPEAAHWCYQAPLLKLAHSVIYK 1080
Db 1021 NLTPFLGIISQASCCYAILKVQNGMTLKASGFPPEAAHWCYQAPLLKLAHSVIYK 1080
Qy 1081 CLLGPLRTAOKLCKLPEATMTILKAAADPALSTDFTOTILD 1122
Db 1081 CLLGPLRTAOKLCKLPEATMTILKAAADPALSTDFTOTILD 1122

RESULT 4

ID ADG90609 standard; protein; 1152 AA.
XX AC ADG90609;
XX DT 25-MAR-2004 (first entry)
XX DE TERT consensus sequence SEQ ID NO:12.
XX KW immune response; telomerase reverse transcriptase; TERT; cytostatic;
XX KW immunostimulant; cancer; cytotoxic T cell response.
XX OS Unidentified.
XX PN WO2004002408-A2.
XX PD 08-JAN-2004.
XX PF 24-JUN-2003; 2003WO-US019844.
XX PR 27-JUN-2002; 2002US-0393295P.
XX PA (GERO-) GERON CORP.

PI Majumdar A, Ferber IA, Frolkis M, Wang Z;
XX WPI; 2004-071946/07.
XX Eliciting an immune response in a mammal specific for its own telomerase
PT reverse transcriptase (TERT), useful for treating or preventing cancer,
PT comprises administering a composition containing TERT of another
PT mammalian species.
XX Claim 10; SEQ ID NO 12; 44pp; English.
XX The invention relates to a novel method for eliciting an immune response
CC in a mammalian subject that is specific for its own telomerase reverse
CC transcriptase (TERT), comprising administering an immunogenic composition
CC containing a protein with at least 20 consecutive amino acids of TERT of
CC another mammalian species, or a nucleic acid encoding the protein. A
CC composition of the invention has cytostatic, and immunostimulant
CC activity. The protein or the nucleic acid encoding the protein is useful
CC in the manufacture of a medicament for the treatment of cancer in a human
CC or for eliciting a cytotoxic T cell response in a human.
XX Sequence 1152 AA;
Qy Query Match 82.3%; Score 4859; DB 8; Length 1152;
Db Best Local Similarity 83.2%; Pred. No. 0;
Matches 959; Conservative 40; Mismatches 122; Indels 32; Gaps 7;
Qy 1 MTRAPRCAPVRLSLRSRYREVWPLATFVRLGDEGRLLVQGPDKIYRTLVAQCLVCMHW 60
Db 1 MPRAPRCRAVRLSLRSRYREVWPLATFVRLGDEGRLLVQGPDPAAFRALVAQCLVCPW 60
Qy 61 GSOPPPADLDFHGVSSIKELVARVQRLCERNERNVLAFGPELLNEARGPPNAPFTSSVR 120
Db 61 GARPPPAAPDFHGVSSIKELVARVQRLCERNERNVLAFGPELLDARGGPPNAPFTTSVR 120
Qy 121 SYLPNTVETLRYSGAWMLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQICA 180
Db 121 SYLPNTVETLRYSGAWMLLSRVGDDLLVYLLAHCALYLLVPPSCAYQVCGSPLYQIGA 180
Qy 181 TTDIWPVSASVYRTPRVGRNFTNLFLOQIKSSROEAPKPLALPSRGTKHLSLTS 240
Db 181 TQARPFPHASGRPRRVPVGRNFTNLGFCERAWNHSVREAGVPLGLPSFGAKRGGASRS 240
Qy 241 VPSAKKARCYVPVRBEGPHQVLPVPSGKSWPSPARSPEVP---TAEKOLSSKGKVS 297
Db 241 LPLPKARRGAAPERTPVGQSWTPSGRTRVPSDAGSPVSPARPAEDLSKGKVS 300
Qy 298 LSLSGSYCCCKHPSS-TSLSPRONAFQLRP-FIETRHFLYSGDGOERLNPFLSLNL 355
Db 301 LSLSGSYCCCKHPSSPPSLSPRPNAFQLRPVVAETKHFLYSYG-GRERLRPSFLLSLNL 359
Qy 356 QPNLTGARRLVEIFLGSRRPTSGPLCRTHLSRRYQWMPFLQOLLVNHAECCOYVLLR 415
Db 360 QPSLTGARLIVETIFLGSRRPTSGPLCRTHLSRRYQWMPFLQELLGNHARCYPVLLR 419
Qy 416 SHCFRTANQVTDALNTSP-----HLMDDLRLHSSPMQVYGF 455
Db 420 SHCPLRAAATPVAGALNTSPQGSVAAPBEVAAPQEQDSTRMLQLRQSSPMQVYGF 479
Qy 456 RACLCCKVVSASLGMTRHNRFFKNLKKFISLGKYKLSLOELMWKVEDCHWLRSPPG 515
Db 480 RACLCCKVVSASLGMTRHNRFFKNLKKFISLGKYKLSLOELMWKVEDCHWLRSPPG 539
Qy 516 KDRVPAAEHRLRERILA---TFLFWLMDTVVQLLSFFFITESTFQKNRLFYRKSVWS 572
Db 540 YESVPAAEHRLRERILAKEHPFLFWLMSVVVELLSFFFITESTFQKNRLFYRKSVWS 599
Qy 573 KLOSIGVROHLRRLRELSQEVRRHQEAWPAMPICRLRPIPKPNGLRPIVNMYSMGT 632
Db 600 KLOSIGVROHLRRLRELSQEVRRHQEAWPAMPICRLRPIPKPNGLRPIVNMYSMGT 659
Qy 633 RALGRRKQAOHFTQRLKTLFSLMNTYRTKHPHLMGSSVLGMDNIYRTWAFVLRLVRLALDQ 692

Db 660 RAFGRKQAHQHTQRLKTLFVSVLNTVETKPHLLGASVLGMNDIYRTWRTFVLRVRLDLP 719
 QY 693 TPRMVFVADVTGAYDAIPQGLVEVAMIRHSESTYCIQYAVVRDSDQOVHKSFR 752
 Db 720 TPRMVFVADVTGAYDAIPQGLVEVAMIRHSESTYCIQYAVVRDSDQOVHKSFR 779
 QY 753 QVTTLSDLQPYNGQFLKHLQSDASALRNSVVEIQSISWNESSSIFDPFLHRSVVK 812
 Db 780 QVTTLSDLQPYNGQFLKHLQSDASALRNSVVEIQSISWNESSSIFDPFLHRSVVK 839
 QY 813 IGDCVTCQCGIPQSSSLTLCSLCFQDMENKLPFAVORDGILLRFVDDFLVTPHLDQ 872
 Db 840 IGRCVTCQCGIPQSSSLTLCSLCFQDMENKLPFAVORDGILLRFVDDFLVTPHLDQ 899
 QY 873 AKTFLSTLVHGVPEYGCMLNKTQVNVFVEPTGLGGAAPYQLPAHCLFPWCGLLDQT 932
 Db 900 AKTFLSTLVHGVPEYGCMLNKTQVNVFVEPTGLGGAAPYQLPAHCLFPWCGLLDQT 959
 QY 933 LEVFCDSGYAQTSTKTSITFQSVKAGTKMTNKLKLLSVLRKCHGLFLDLQNSLQTVCI 992
 Db 960 LEVFCDSGYARTSIKASITFORVFKAGKNMENKLLSVLRKCHSLFLDLQNSLQTVCI 1019
 QY 993 NIYKIFLLQAVFPHACVTLQDPQVRKNLTFFLGIISQASCCYAILKVNPGMTLK-- 1050
 Db 1020 NIYKIFLLQAVFPHACVTLQDPQVRKNLTFFLGIISQASCCYAILKVNPGMTLKAK 1079
 QY 1051 --ASGSFPPPEAAHWLCYQAFLLKLAHSHVYKCLLGLPLRTAQKLCRKLPEATMTILKAAA 1109
 Db 1080 GNAGSFPPPEAAHWLCYQAFLLKLAHSHVYKCLLGLPLRTAQKLCRKLPEATMTILEAAA 1139
 QY 1110 DPALSTDFQTILD 1122
 Db 1140 DPALSTDFQTILD 1152
 RESULT 5
 ADD21416
 ID ADD21416 standard; protein; 1128 AA.
 XX AC ADD21416;
 XX DT 15-JAN-2004 (first entry)
 XX DE Golden hamster TERT protein related to continual cell growth.
 XX KW continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;
 KW cdk6; activating mutation; cell growth; cell division; cell cycle;
 KW cancer-causing agent; continual growth-induced cell; enzyme; TERT;
 KW telomerase; Golden hamster.
 XX OS Mesocricetus auratus.
 XX FN WO2003044169-A2.
 XX PD 30-MAY-2003.
 XX PF 15-NOV-2002; 2002WO-US036729.
 XX PR 15-NOV-2001; 2001US-0334760P.
 XX PA (UTEM) UNIV TEMPLE.
 XX PI Reddy PE, Rane SG, Mettuss RV;
 XX WPI; 2003-449813/42.
 XX A composition for reversibly inducing continual growth in normal cells
 PT comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or
 PT its active fragment, derivative, homolog or analog, having an activating
 PT mutation.
 XX XX
 XX Disclosure; Page 119-121; 77pp; English.

CC This invention relates to a novel composition for inducing a reversible
 CC state of a continual growth in cultured cells and comprises at least one
 CC compound comprising a cyclin dependent kinase (cdk)4, cdk2 or cdk6
 CC protein having an activating mutation. Growth and division of living
 CC cells involve a regular series of events and processes that comprise the
 CC cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in
 CC the control of G1, the point at which cells irrevocably commit to DNA
 CC synthesis and thus enter the cell cycle. The invention is useful in
 CC reversibly inducing continual growth in normal cells and may allow the
 CC screening of cancer-causing agents with the continual growth-induced
 CC cells. The present sequence is that of the golden hamster TERT protein.
 CC the catalytic subunit of telomerase, related to the invention. Note: Due
 CC to an error in the specification or sequence listing, the Seq ID numbers
 CC given in the disclosure do not correspond to those given in the sequence
 CC listing. It is therefore unclear which Seq ID number corresponds to which
 CC sequence and exactly which sequence is being claimed.

SQ Sequence 1128 AA;

Query Match 80.5%; Score 4751; DB 7; Length 1128;
 Best Local Similarity 80.1%; Pred. No. 0;
 Matches 904; Conservative 90; Mismatches 127; Indels 8; Gaps 4;

QY 1 MTRAPRCDAVRSLLSRYREYVWPLATFVRRLLGPEGRRLVQDPDKIYRTLVACLVCHHW 60
 Db 1 MPRAPRCRAVALLRSQYRQVWPLATFVRRLLGPEGRQLVQDPDKVFTLVARCLVCPW 60
 QY 61 GSQPPPADLSFHQVSSSLKELVARVVQRLCERNERNVLAFFPELLNEARGPMPMAFTSSVR 120
 Db 61 DSQPPPADLSFHQVSSSLKELVARVVQRLCERNERNVLTGFFALLNGAOGGPPMTTTSVR 120
 QY 121 SYLPTNTVITLVRSGAMLLLSRVGDDLLVYLLAHFALYLLVPPSCAYQVCGSPLYQICA 180
 Db 121 SYLPSNVSTESLRVSGAMLLLNRYGDDLLVYLLARFALYLLVPPSCAYQVCGSPLYQICA 180
 QY 181 TTDIWPVSASVYRTPRVGRNPTNLRFLQTKSSSRQEAPELALPSRGTKHLSLTSTS 240
 Db 181 TAETWPSVSRIYRTPRVGRNPTNLRFLQTKSSSRQEAPELALPSRGTKHLSLTSTS 240
 QY 241 VPSAKKARCVPRVVEGPHRQVLTPTSGKSWPSPARSPVP--TAEKDLSSSGKVSD 297
 Db 241 VPPSKARCDLAPLEKGYRQAVPTPSDKTWPNPAKSHAVFSRTTKEDLSSGVKAPG 300
 QY 298 LSLSGSVCKHKPSTSLSPRQNAFQRLPFIEITHFLYSGRGGQERLNPFLSNLQP 357
 Db 301 LSRSGSVCKHKPSTSLSPRQNAFQRLPFIEITHFLYSGRGGQERLNPFLSNLQP 360
 QY 358 NLTGARLVEIIFLGSRRPTSGPLCRTHLSRRVWQRPPLFQOLLVNHACQYVRLRSH 417
 Db 361 SLTGARLVEIIFLGMRRPTSGPLCGRRRLSKRYQWRPLFQOLLVNHARCPYVRLRSH 420
 QY 418 CRFTANQOQVTDALN-TSPPHLMDLLRLHSSPWQVYGFRLACLCVVSASLWGTNRNRR 476
 Db 421 CRFTANQOQVAGALNTTSPQRLMMLLLHSSPWQVYGFRLACVGLVPPGLWGRSHNRR 480
 QY 477 FFKNLKRPISLGYKLSLQELMWKQVDECHWLRSSPGKDRVPAAEHRLRERILATFLP 536
 Db 481 FFKNVKRPISLGYKLSLQELTWKMKVQDCRWLRSSPGNNCVPAAEHRTREIRILAVFLP 540
 QY 537 WMDTYVQVLLRSPFYITESTFQKRLPFPYKKSWSKLSQISGVQHLRRLRLRSLQSEV 596
 Db 541 WMDAYVVELLRSPFYITETTFQKRLPFPYKKSWMRLQSIGVRHHLRRLRLRSLQSEV 600
 QY 597 RHODTWMALPDCRLRFPKPNGLRPIVNMYSYMGTRALGRKQAHQHTQRLKTLFMSLN 656
 Db 601 RQRQEPAMPAPICRLRFIPKSPGRPIVNMYSY-MGTRAFDGRKQAHQHTQRLKTLFMSLN 659
 QY 657 YERTKHPHLMGSSVLGMNDIYRTWRAFLVRLALDQTPRMTYFVKADVTGAYDAIPQGLV 716
 Db 660 YELTKHTNLLGASVLGNDIYRTWRTFVLVRLDPAPEMYFVKADVTGAYDAIPQGLV 719
 QY 717 EVVANMIRHSESTYCIQYAVVRDSDQOVHKSFRQVTTLSDLQPYNGQFLKHLQSDA 776

Db 720 EVIANMIRHPDNSYCIHQYAVVQRDRQGIHKSFRRQVSTLSDLQPHMGQFLKHLQSDT 779
Qy 777 SALRNSVVEIOSISWNESSSLPFFFLPLRHSVVKIGDRCYTCOGIPQSSSLTLLCS 836
Db 780 SALRNSVVEIOSLSLNEASSLPFFFLFRVNSVVKIGRCYVQCQIPQSSSLTLLCS 839
Qy 837 LCFGDMENKLFABVQRDGLLRFVDDFLVTPHLDQAKTFLSLTVHGVPEYGCMINLQKT 896
Db 840 LCFGDMENKLFABVQDGLLRFVDDFLVTPHLDQAKTFLSLTVHGVPEYGCMINLQKT 899
Qy 897 VVNFPEVETLGGAPYOLPAHCLFPMCGLLDQTLEVFCDYSGYAQTSIKTSLTFQSV 956
Db 900 VVNFPEVADGTLDTAPHLQPAHCLFPMCGLLDQTLEVLCDYTGARTSIKSLTFQRT 959
Qy 957 FKAGKTRNKLVSURLKCHGLFLDLQVNSLQTVICINIKYKIFLQAVRPHACVQLPDPQ 1016
Db 960 FKAGRNMRQKLLAVLRLKCHSLFLDLQVNSLQTVICINIKYKIFLQAVRPHACVQLPDPQ 1019
Qy 1017 RVRKNLTPFLGIISSQASCCYAILKVNPGWTLK---ASSGSPFPEAAHWLCYQAFLLKLA 1073
Db 1020 HVRKNPAPFLSIINIASCCYSILKVNAGWTLKAKAGSGSPFPEAAHWLCYQAFLLKLA 1079
Qy 1074 AHSVIYKCLLGLRLTAQKLCRKLPEATMTILKAAADPALSTDFQTILD 1122
Db 1080 GHSVYKCLLGLRLTAQKLCRKLPRATWAILETAADPALSTDFQTILD 1128

RESULT 6
ADG90603
ID ADG90603 standard; protein; 1128 AA.

XX AC ADG90603;

XX DT 25-MAR-2004 (first entry)

XX DE Hamater TERT SEQ ID NO:6.

XX KW hamster; immune response; telomerase reverse transcriptase; TERT;
XX KW cytosolic; immunostimulant; cancer; cytotoxic T cell response.

XX OS Mesocricetus auratus.

XX PN WO2004002408-A2.

XX PD 08-JAN-2004.

XX PF 24-JUN-2003; 2003WO-US019844.

XX PR 27-JUN-2002; 2002US-0393295P.

XX PA (GERO-) GERON CORP.

XX PI Majumdar A, Ferber IA, Frolkis M, Wang Z;

XX DR WPI; 2004-071946/07.

XX DR N-PSDB; ADG90602.

XX PT Eliciting an immune response in a mammal specific for its own telomerase
XX PT reverse transcriptase (TERT), useful for treating or preventing cancer,
XX PT comprises administering a composition containing TERT of another
XX PT mammalian species.

XX PS Claim 10; SEQ ID NO 6; 44pp; English.

XX The invention relates to a novel method for eliciting an immune response
XX in a mammalian subject that is specific for its own telomerase reverse
XX transcriptase (TERT), comprising administering an immunogenic composition
XX containing a protein with at least 20 consecutive amino acids of TERT of
XX another mammalian species, or a nucleic acid encoding the protein. A
XX composition of the invention has cytostatic, and immunostimulant
XX activity. The protein or the nucleic acid encoding the protein is useful
XX in the manufacture of a medicament for the treatment of cancer in a human
XX or for eliciting a cytotoxic T cell response in a human.

XX SQ Sequence 1128 AA;
Query Match 80.5%; Score 4751; DB 8; Length 1128;
Best Local Similarity 80.1%; Pred. No. 0;
Matches 904; Conservative 90; Mismatches 127; Indels 8; Gaps 4;
Qy 1 MTRAPRCPAVRSLLRSRYREVWPLATFVRRLGPEGRRLVQGPDKIYRTLVQAQCLVCMHW 60
Db 1 MPAPRCRAVALLRSQYRVQVWPLATFVRRLGPEGRRLVQGPDKIYRTLVQAQCLVCMHW 60
Qy 61 GSOPPPADLSFHQVSSLSKELVARVQRLCERNERNVLAFCGELLNEARGGPPMAFTSSVR 120
Db 61 DSQPPPADLSFHQVSSLSKELVARVQRLCERNERNVLAFCGELLNEARGGPPMAFTSSVR 120
Qy 121 SYLPNTVETLRVSGAWMLLSRVGDDLLVYLALAHACALYLLVPPSCAYQVCGSPLYQICA 180
Db 121 SYLPNSVTESLRVSGAWMLLSRVGDDLLVYLALAHACALYLLVPPSCAYQVCGSPLYQICA 180
Qy 181 TTDIWPSVSASVYRPTRPVGRNFTNLRFLOQIKSSSROEAPKPLALPSRGTKRHLSTSTS 240
Db 181 TASTWPSVSIYRPTRPVGRNFTNLRFLOQIKSSSROEAPKPLALPSRGTKRHLSTSTS 240
Qy 241 VPSAKKARCYFVPRVEGPHRQVLPTPSGKSWPSPARSPEVP---TAEKDLSSGKQVSD 297
Db 241 VPSKAKARCDLAPRLEKGPYRQAVPTESDKTWVPNPAKSHAVPISTRTTKEDLSSGKQVSD 300
Qy 298 LSLSGSVCCGKPSSTLSLSPRONAFQRLPFTIETRHFLYSRGDQRRINLPSFLLSNLOP 357
Db 301 LSRSGSVCYKHKPSSTLSLSPRONAFQRLPFTIETRHFLYSRGDQRRINLPSFLLSNLOP 360
Qy 358 NLATGARELVEIIFLGRSPTSGPLCRTHLSRRYQWQRPFLQQLLVNHAECQVYRLLRSH 417
Db 361 SLTGARKLVEILFLGMRPTSGPLCGRRRLSKRYQWQRPFLQQLLVNHAECQVYRLLRSH 420
Qy 418 CRFRTANQVTDALN-TSPPHLMDLLRLHSSPMQVYGFRLACLCCKVVSASLWGTNRHRR 476
Db 421 CRFRTAAHQVAGALNTTSPQRLANLLRLHSSPMQVYGFRLACLCCKVVSASLWGTNRHRR 480
Qy 477 FFKNLKFIISLGKYGKLSLQELMWKMKVEDCHLRSSPGKDRVPAAEHLRERILANFLP 536
Db 481 FFKNVRFIISLGKYDKLSLQELTWQMKVQDCRLRSSPGNNCVPAEHLRERILANFLP 540
Qy 537 WLMDTVYVQLLRSPFFYITESTFQKRLFFYKRSVMSKLSQIGVQRHLERLRLSREB 596
Db 541 WLMDAYVVELLRSPFFYITESTFQKRLFFYKRSVMSKLSQIGVQRHLERLRLSREB 600
Qy 597 RHHQDTWLAMPICRLRFIPKPNGLRPIVNMYSNGTALGRRKQAQHTQRLKTLFSLN 656
Db 601 RQREAWPAMPICRLRFIPKPSGLRPIVNMYS-MGTRAFDKQAQHTQRLKTLFSLN 659
Qy 657 YERTKPHLMGSSVLGNDIYRTWRAPVLVRALDQTPRMVFKADVGTAYDAIPQDKLV 716
Db 660 YELTKHTNLGASVLGLNDIYRTWRTEVLRVRLDPAFRMYFKADVGTAYDAIPQDKLV 719
Qy 717 EVVANMIRHSESTYCIROYAVVRRDSQGVHKSPRRQVTTLSDLQPYMGQFLKHLQSDA 776
Db 720 EVIANMIRHPDNSYCIHQYAVVQRDRQGIHKSFRRQVSTLSDLQPHMGQFLKHLQSDT 779
Qy 777 SALRNSVVEIOSISWNESSSLPFFFLPLRHSVVKIGDRCYTCOGIPQSSSLTLLCS 836
Db 780 SALRNSVVEIOSLSLNEASSLPFFFLFRVNSVVKIGRCYVQCQIPQSSSLTLLCS 839
Qy 837 LCFGDMENKLFABVQRDGLLRFVDDFLVTPHLDQAKTFLSLTVHGVPEYGCMINLQKT 896
Db 840 LCFGDMENKLFABVQDGLLRFVDDFLVTPHLDQAKTFLSLTVHGVPEYGCMINLQKT 899
Qy 897 VVNFPEVETLGGAPYOLPAHCLFPMCGLLDQTLEVFCDYSGYAQTSIKTSLTFQSV 956
Db 900 VVNFPEVADGTLDTAPHLQPAHCLFPMCGLLDQTLEVLCDYTGARTSIKSLTFQRT 959
Qy 957 FKAGKTRNKLVSURLKCHGLFLDLQVNSLQTVICINIKYKIFLQAVRPHACVQLPDPQ 1016
Db 960 FKAGRNMRQKLLAVLRLKCHSLFLDLQVNSLQTVICINIKYKIFLQAVRPHACVQLPDPQ 1019

Db 960 FXAGRNMRKGLAVLRKCHSLFLDLQMSLQTVNCVYKIFLQAYRFHACALQPPDQ 1019
 QY 1017 RVKRLTFFLGIISQASCCYAILKVNPKWTILK---ASGSPPEAAHWLVCYQAFLLKLA 1073
 Db 1020 HVEKNPAFFLSIISNTASCCYSILKYNAGWTLKAGGSGSPPEAAHWLVCYQAFLLKLA 1079
 QY 1074 AHSVYKCLLGLPRTAQKLLCRKLPEATWTILKAAADPALSTDFQILD 1122
 Db 1080 GHSVYKCLLGLPRTAQKLLCRKLPEATWTILKAAADPALSTDFQILD 1128

RESULT 7
 AAW46957
 ID AAW46957 standard; protein; 1132 AA.
 AC AAW46957;
 XX
 DT 13-AUG-1998 (first entry)
 XX
 DE Human telomerase reverse transcriptase.
 KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 KW cell proliferation; cancer; ageing; ribonucleoprotein.
 XX
 OS Homo sapiens.
 XX
 PN GB2317891-A.
 XX
 PD 08-APR-1998.
 XX
 PF 01-OCT-1997; 97GB-00020890.
 XX
 PR 01-OCT-1996; 96US-00724643.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912951.
 PR 14-AUG-1997; 97US-00915503.
 XX
 PA (GERO-) GERON CORP.
 PA (UYTS-) UNIV TECHNOLOGY CORP.
 XX
 PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 XX
 DR WPI; 1998-171633/16.
 DR N-PSDB; AAW22379.
 XX
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX
 PS Claim 3; Fig 17; 387pp; English.
 XX
 CC The present sequence represents human telomerase reverse transcriptase
 CC (hTERT), which is a ribonucleoprotein. The present invention also
 CC describes the following methods: (A) determining whether a test compound
 CC is a modulator of hTERT, by detecting the change in hTERT recombinant
 CC protein or polynucleotide, on administration of the compound; (B)
 CC preparation of recombinant telomerase by contacting a protein preparation
 CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
 CC protein in a sample by binding a relevant probe to the sample and
 CC detecting the complex formed or in the case of RNA detection, amplifying
 CC the product and correlating the presence of complex or amplification
 CC product with presence of hTERT in the sample; and (D) increasing the
 CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
 CC the use of an agent that causes an increase in cell vertebrate cell
 CC proliferation to create a medicament that inhibits ageing. A protein
 CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
 CC the manufacture of medicaments for inhibiting the effect of ageing or
 CC cancer. Inhibitors of telomerase activity can be used to treat conditions

CC that are associated with high telomerase activity. A protein preparation
 CC of hTERT can also be used in the new methods

SQ Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 2; Length 1132;
 Best Local Similarity 62.4%; Pred. No. 0;
 Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

QY 1 MTRAPRCAPVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPDGPKIYRTFLVAQCIVCMHW 60
 Db 1 MPRAPRCAPVRSLLRSRYREVWPLATFVRRLGPEGRRLVQPDGPKIYRTFLVAQCIVCMHW 60
 QY 61 GSQPPADLSFHQVSSSLKELVARVVRQRCERNRNLAFGPFELLNEARGGPPMAFTSSVR 120
 Db 61 DARPPPAAPSFRQVSCVCLKELVARVVRQRCERNRNLAFGPFELLNEARGGPPMAFTSSVR 120
 QY 121 SYLPTNTVETLRVSGAWMLLSRVGDDLLVYLLAHCALVLLVPPSCAYQVCSPLYQICA 180
 Db 121 SYLPTNTVETLRVSGAWMLLSRVGDDLLVYLLAHCALVLLVPPSCAYQVCSPLYQICA 180
 QY 161 TTDIWPSVSASVYRTPVGRNFTNLFLOIKSSSRQEAQPLALPSRGTKRHLSLTSTS 240
 Db 161 ATQARPPPHAS-GPRRLG-----CERAWNHSVREAGVPLGLPAPCARRGGSASRS 231
 QY 241 VPSAKKARCYVPVRVEEGF-----HRQVLPTPSGKSW-VPSPARSPSEVPTAEKDLSSK 292
 Db 232 LPLPKRPRGAAPBEPRTVGGGSAWHFGRTRGSDRGFCVVSAPAR-----PAEATSLE 286
 QY 293 GKVDLSLS-GSVCKHKPSSTLSLSPRONAQFLRP-FIETRHFLYSGDQGRINPSF 350
 Db 287 GALSGRHSHPSVGRQHAGPPSTSRPRPMDTTPCPVVAETKFLYSSGD-KEQLRPSF 345
 QY 351 LLSNLOPNLTGARLVEIIFLGSRRPTSGPLCRTHLSRRYQWMPPLFCOLLVNHACQY 410
 Db 346 LLSLRPLSLTGARLVETIFLGSRRPMPGTPRRLPRLPQRYQWMPPLFLELLGNHAQCPY 405
 QY 411 VRLLSRCHCRFTANQQVTDAL-----NTSPPHMLDLLRLHSSPWOVY 452
 Db 406 GVLLKTHCPLEAA---VTPAAGVCAREKPGQSVAAPEEDTDPRLLVQLLRQSSFPQVY 462
 QY 453 GFLRACLCVVSASLWGTTRHNRFFKNLKKFISLGKYGKLSLQELMWMKVEDCHWLRS 512
 Db 463 GFVRACLRLVPPGLWGSRHNRFFLNRTKKFISLGKHAQLSLQELTWKMSVRDCAWLR 522
 QY 513 SPGKDRVPAAEHRLAERILATFLWMDTYVOLLRSFFYITESTFQKRLPFYKRSVMS 572
 Db 523 SPGVGCVPAAEHRLAERILATFLWMDTYVOLLRSFFYITESTFQKRLPFYKRSVMS 582
 QY 573 KLSQIGVROHLERVRLRELSOEVRHODTWLAMPICRLRFPKNGRLRPIVNMYSWGT 632
 Db 593 KLSQIGVROHLERVRLRELSOEVRHODTWLAMPICRLRFPKNGRLRPIVNMYSWGT 642
 QY 633 RALGRKQAOHFTQRLKTLFSMANYERTKPHLMGSSVGLMNDIYRTWRAFLVRALDQ 692
 Db 643 RTFRREKKAERLTGRVLFVNLVYERARRPCLLGASVLGLDDIHRAWRTFVLVRAQDP 702
 QY 693 TPRMVFVADYTGADALPOKLVVVVANMTRHSESTYCIQYAVVRDSDSQGVHKSFR 752
 Db 703 PPFLYFVKVDYTGADYDTPQDRLTEVIAIHK-PQNTYCVRYAVVQAAHGHVRAKPKS 761
 QY 753 QVTTLSDLQPYMGQFLKHLQSDASALRNSVVVQSIQSIQSIQSIQSIQSIQSIQSIQSI 812
 Db 762 HVSITLDLQPYMGQFLKHLQSDASALRNSVVVQSIQSIQSIQSIQSIQSIQSIQSIQSI 819
 QY 813 IGDCRYTCQCGIQGSSSLTLLCSLCFGDMENKLFPAEQVRDGLLRLRVDDLLVTPHL 872
 Db 820 IRGKSYVQCGIQGSSSLTLLCSLCFGDMENKLFPAEQVRDGLLRLRVDDLLVTPHL 879
 QY 873 AKTFLSTLVHGVPEYGCINOKTVNPPVPPGTLGGAAPYQLPAHCLFPWCGLLLDQT 932
 Db 880 AKTFLSTLVHGVPEYGCINOKTVNPPVPPGTLGGAAPYQLPAHCLFPWCGLLLDQT 939

Qy	933	LEVCFDYSYGVAQTSIKTSLTFQSVFKAGKTWRNKLLSVLRKCHGLFLDLQVNSLQTVC	932
Db	940	LEVQSDYSYARTSIRASLTFNRGFKAGRNRRKLFGLRLKCHSLFLDLQVNSLQTVC	939
Qy	993	NIYKIELLQAVRFHACVQLPEQDVRKNIITFFELGIISQASCCYALTKVKNPGMTLKAS	1052
Db	1000	NIYKIELLQAVRFHACVQLPFHQVWKNPTFFELVISTFASLCYSILKAKNAGMSLGAK	1059
Qy	1053	GS---FPPEAAHWLCYQAFLLKLAHSHVYKCLGLPURTAKLCKRLCPBATMTILKAAA	1109
Db	1060	GAAGPLFSEAVQMLCHQAFLLKLTNRHVTVYVPLGLSLRTAQTLQSRKLPGLTTLTALEAAA	1119
Qy	1110	DPALSTDFQITLD	1122
Db	1120	NPALPSDFKTILD	1132

RESULT 8

RESUL 8
AAW90251
ID AAW90251 standard; protein: 1132 AA.

AC AAW90251;

XX
DT 24-MAY-1999 (first entry)XX
DE Human catalytic telomerase sub-unit protein.

xx Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay;
 KW modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
 KW ageing; antisense; neoplastic cell; telomerase-related condition;
 KW tumour cell.

XX
OS Homo sapiens.

XX PN WO9859040-A2.

XX
PD
30-DEC-1998.XX
PF 09-JUN-1998; 98WO-EP003468.XX
PR 20-JUN-1997; 97DE-01026329.

PR 26-MAR-1998; 98DE-01013274.
PR 14-APR-1998; 98DE-01016496.

XX
PA (FARB) BAYER AG.

XX PI Hagen G, Siegmund

XX
DR WPI: 1999-081276/07.

DR N-PSDB; AAV/2117.
XX

PT New catalytically
PT modulation of tel
PT modulation of tel

PT ageing.

W. S. 1000

xx

CC This sequence represents a novel human catalytic telomerase sub-unit

(mRNA). This protein can be used in screening assays to identify modulators of telomerase and to treat or inhibit cellular disorders, death, defects and/or other pathological processes involving telomerase particularly cancer and ageing (also suitable for this are agents that stimulate, inhibit or mimic the activity of the subunit). Antisense nucleic acids inhibit telomerase action (by binding to specific mRNA), particularly in neoplastic cells and may be expressed *in vivo*. Antibodies and fragments of the protein, used as probes or primers, are used to diagnose telomerase-related conditions (especially neoplasia) by (i) detecting abnormal levels of the subunit protein in body fluids or tissues or (ii) by measuring the amount of the encoding nucleic acid. Expression of the nucleic acid encoding the subunit mRNA is confined to tumour cells, in contrast to the ubiquitous expression of the telomerase RNA subunit.

XX

59.4%;	Score	3505;	DB	2;	Length	1132;
62.4%;	Pred.	No.	0;			
719;	Conservative	122;	Mismatches	260;	Indels	52;
Gap						
1	MT	R	A	P	C	P
1	MP	R	A	P	C	R
61	G	S	O	P	P	A
61	D	A	R	P	P	A
121	S	Y	L	P	T	V
121	S	Y	L	P	T	V
181	T	T	D	I	N	S
181	A	T	O	A	R	P
241	V	P	S	A	K	A
232	L	P	I	P	K	P
293	G	K	V	S	D	L
287	G	A	L	S	G	T
351	L	L	N	Q	P	N
346	L	L	S	R	P	S
411	V	L	L	R	S	H
406	G	V	L	L	T	H
453	G	F	R	A	C	L
463	G	F	V	R	A	C
513	S	P	G	K	O	R
523	S	P	G	V	C	P
573	K	L	O	S	I	G
583	K	L	O	S	I	G
633	R	A	L	G	R	R
643	R	T	F	R	E	K
693	T	P	R	M	F	V
703	P	P	E	L	F	V
753	Q	V	T	T	L	S
762	H	V	S	T	L	D
813	I	G	D	R	C	Y
820	I	R	G	S	Y	V
873	A	K	T	F	L	S
880	A	K	T	F	L	R
933	L	E	V	F	C	D
940	L	E	V	O	S	D

Qy	1053	GS----	FPPEAAHWLCYQAPFLKLAHSHVIYKCLIGPLRTAQKLCRKLPKATMTILKAAA	1109
		:		:
Db	1060	GAAGPLPSEAQWLCHQAFLLKLT	TRHRVTYVPLIGSLRTAQQLSRKLPGLTTLTALSA	1119
		:		:
Qy	1110	DPALSTDPQTILD	1122	
		:		:
Db	1120	NPALPSPDKTILD	1132	
RESULT 10				
Id	AA32090	standard; protein; 1132 AA.		
Xx	AA32090;			
Xx	17-JAN-2000	(first entry)		
Xx	Human telomerase reverse transcriptase (hTERT).			
Xx	Telomerase reverse transcriptase; human; hTERT; cell proliferation; cancer.			
Kw				
Xx	Homo sapiens.			
Xx	W0950386-A2.			
Pw				
Xx	07-OCT-1999.			
Pd				
Xx	31-MAR-1999;	99WO-US007097.		
Pp				
Xx	31-MAR-1998;	98US-00052864.		
Px				
Pr	03-AUG-1998;	98US-00128354.		
Pf				
Xx	(GERO-) GERON CORP.			
Pa				
Pi	Morin GB;			
Pt				
Dp	WPI; 1999-610842/52.			
Dr	N-PSDB; AA220279.			
Xx	New catalytic polypeptide and polynucleotide, useful for increasing catalytic activity in a cell.			
Pt				
Pf				
Xs	Claim 13; Fig 1; 24pp; English.			
Pf				
Xx	The present sequence represents human telomerase reverse transcriptase (hTERT). Human telomerase is a target for diagnosing and treating diseases relating to cell proliferation and senescence, such as cancer, or for increasing the proliferative capacity of a cell. A claimed method for increasing the proliferative capacity of a vertebrate cell, especially a human or other mammalian cell, involves introducing into the cell a recombinant hTERT polynucleotide encoding an hTERT variant in which residues 192-323, 200-323, 192-271, 200-271, 222-240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 of the present sequence are deleted. A claimed method of preparing recombinant telomerase involves contacting a recombinant hTERT deletion mutant (as above) with a telomerase RNA component such that the 2 proteins associate to form a complex capable of catalyzing the addition of nucleotides to a telomerase substrate. A claimed method for reducing telomerase activity in a cell involves introducing a recombinant polynucleotide encoding an hTERT variant having a deletion of amino acids 192-450, 560-565, 637-660, 748-764 or 1055-1071 of the present sequence			
SQ	Sequence 1132 AA;			
Query Match				
Best Local Similarity		59.4%;	Score 3505;	DB 2; Length 1132;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;				
Qy	1	MTRAPRCVRSLLRSRREVWPLATFVRRLLGPEGRRLLVQPDPKIYRTLVAQCLVCMHW	60	
Db	1	MPRAPRCVRSLLRSRREVWPLATFVRRLLGPEGRRLLVQPDPAAPRALVAQCLVCPW	60	

Qy	61	GSOPPPADLSFHVSSIKELVARVWORLCEBNNRNLAFGFLINERAGGPPMAFTSSVR	120
Db	61	DARPPAAPSPFQVSCLELVARVQRLCERGAKNVLAFCFALLDARGGPPFAFTTSVR	120
Qy	121	SYLPNTVETLRVSGAWMLLSRVGDDLLVYLAHACALYLLVPPSCAYQVCGSPYQICA	180
Db	121	SYLPNTVTDALRGSGAWMLLSRVGDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA	180
Qy	181	TTDIWPSVASYRPTRPVGRNFTNLRFLOQIKSSSQEAPKPLALPSRCTYKHLSTSTS	240
Db	181	ATQARPPPHAS-GPRRRLG-----CERAWNHSVREAGVPLGLPAGARRRGGSASRS	231
Qy	241	VPSAKKARCYVPVRVEGP-----HROVLPTPSGKSM-VPSPARSPVEPTAKDKLSK	292
Db	232	LPLPKRPRRGAAPERTPVGQSGSWAHGTRGSPDRGFCVSPAR-----PAEATSLB	286
Qy	293	GKVSLSLS-GSVCKHKPSSTLSLGPQNAFOLRP-FIETRHFLYSGRGQRLNPSF	350
Db	287	GALSGTRHSHPSVGRQHAGPPSTSRPPRPWDTPCPDVAETKHFLYSSGD-KEQLRPSF	345
Qy	351	LLSNLQNLTGARLVEIIFLGSRPRTSGPLCRHLSRBYWQMRPLFOQLLVNHAECQY	410
Db	346	LLSSRLPSLTGARRLVETIFLGSRPMPGTPRLPLPQRYWQMRPLFLELLGNHACQPY	405
Qy	411	VLLRSHCRFTANQQVTDAL-----NTSPPHLMDLLRLHSSPMQVY	452
Db	406	GVLLKTHCPLRAA---VTPAAGVCAREKPOGSVAAPSEEDTDPRLLVQLLRQHSPPQVY	462
Qy	453	GFLRACLCKVVSASLNGTRNERRFFKXKFTSLGKYKLSLOELMKMKVEDCHWLRS	512
Db	463	GFVRACLRLVPPCLWGSRNERRFLRNTKFTSLGKHAKLSLOELTKWMSVRDCAWLRR	522
Qy	513	SPGKDRVPAAEHLRERILATFLWMDTVVOLLRSFFVITESTFOKRLFFYKKSWS	572
Db	523	SPGVGCVPAAEHLRERELAKFLHLMSSVVVVELLSFFVYVTFTFOKNRLFFYKKSWS	582
Qy	573	KLOSIGVROHLRVLRLSQQEVRHODTWLAMPICRLRFIPKPNGLRPIVNNSSYSGT	632
Db	583	KLOSIGIRQHLKRVQLRESEAEVRQREARPPALLTSRLRPIPKPDGLRPIVNDVVYGA	642
Qy	633	RALGRKQAOHFTORLKTFLSMLNYERTKPHLMGSSVLGMDIYRTWRAPVLVRALDQ	692
Db	643	RTPEREKRAELTSRVKALFSLNYERARRPGLLGASVLGLDDIHRARWTFVLVRADP	702
Qy	693	TPRMVFKADVGTAYDAIPOGKLVSVVANNIRHSESTYCIROYAVVRDSOGQVHKSPRR	752
Db	703	PELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PONTYCVRRYAVVOKAAHGHVRKAFKS	761
Qy	753	QVTTLSLQPMVGQFLKHLQSDASALRNSVVIQSI SMNNESSSLDFDFLHFLRHSYVK	812
Db	762	HVSTLTDLQPMRQFVAHLET--SPLRDAVVIQSSSLNEASSGLFDVPLRFCHHAVR	819
Qy	813	IGRCYTCQCGIPQSSSLTLLCSLCFQDMENKLFASVQRDGLLLRVDDFLVTPHLQD	872
Db	820	IRGKSYVQCQIPQSSILTLLCSLCYGD MENKLFAGIRRDGLLLRLVDDFLVTPHLTH	879
Qy	873	AKTFSLTVHGVPYGCWMLNOKTVNPFVPGTGLGNAAPVQLPAHCLFPMCGLLDQT	932
Db	880	AKTFRLTVRGVPYGCWMLNOKTVNPFVDEALGGTAFVQMPAHGLFFPMCGLLDRT	939
Qy	933	LEVPCDYGVAOTSITKTSLTFQSVFKAGKTRNKLKLSVLRKCHGLFLDLQVNSLQTVCI	992
Db	940	LEVQSDYSSVARTSIRASLTFNRGCFKAGRNWRKLFVGLRLKCHSLFLDLQVNSLQTVCT	999
Qy	993	NIYKIFLLQAYRFHACVQLPFDQVRNKLTPFGIIGIISQASCCYAILKVQXPGMTLKAS	1052
Db	1000	NIYKILLQAYRFHACVQLPFPHQVQWKNPFFFLRVISDTASLCYSILKAKNAGSLGAK	1059
Qy	1053	GS----FPPEAAHWLCYQAPFLKLAHSHVIYKCLIGPLRTAQKLCRKLPKATMTILKAAA	1109
Db	1060	GAAGPLPSEAQWLCHQAFLLKLT	1119

QY	1110	DPALSTDFQTILD	1122	
DB	1120	NPALPSDFKTILD	1132	
RESULT 11				
AY43621				
ID	AY43621	standard; protein; 1132 AA.		
XX	AY43621;			
XX	26-JAN-2000	(first entry)		
DE	A human telomerase reverse transcriptase (TRT) polypeptide.			
KW	Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;			
KW	dendritic cell; telomerase activity; cancer cell; proliferating cell;			
KW	immunological destruction; telomerase; cancer; proliferation disease.			
OS	Homo sapiens.			
XX	WO9950392-A1.			
XX	07-OCT-1999.			
XX	30-MAR-1999;	99WO-US006898.		
XX	31-MAR-1998;	98US-0112006P.		
PA	(GERO-) GERON CORP.			
PI	Gaeta FCA;			
DR	WPI; 1999-610845/52.			
DR	N-PSDB; AA230154.			
PT	Eliciting an in vivo immune response for prevention and treatment of			
PT	cancers.			
XX	Claim 3; Fig 1; 26pp; English.			
CC	The present sequence represents a human telomerase reverse transcriptase			
CC	(TRT) polypeptide. The protein is used in the method of the invention.			
CC	The specification describes a method for activating a T lymphocyte,			
CC	comprising contacting the T lymphocyte with a dendritic cell that			
CC	expresses a TRT peptide in the context of a MHC class I or MHC class II			
CC	molecule. The protein causes induction of an in vivo immunological			
CC	response to telomerase activity. Cancer cells are characterized by			
CC	expression of endogenous TRT gene and the presence of detectable			
CC	telomerase activity. Therefore, by eliciting a specific immune response			
CC	to TRT or to TRT-expressing cells, it is possible to selectively target			
CC	proliferating cells for immunological destruction. The method is used for			
CC	eliciting an in vivo immune response to telomerase by activating a T			
CC	lymphocyte, and is useful for prevention and treatment of cancers and			
CC	other proliferation diseases/conditions			
XX	Sequence 1132 AA;			
Query Match				
Best Local Similarity 59.4%; Score 3505; DB 2; Length 1132;				
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;				
QY	1	MTRAPRCAPVRSLLRSRYREVWPLATFVRLGPEGRRVQPGDKPIYRLVAQCLVCMHW	60	
DB	1	MTRAPRCARVRSLLRSRYREVWPLATFVRLGPEGRRVQPGDKPIYRLVAQCLVCMHW	60	
QY	61	GSQPPADLSFQVSSKLKELVARVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120	
DB	61	DARPPAPSPFQVSSKLKELVARVQRLCERNERNVLAFGFELLNEARGGPPMAFTSSVR	120	
QY	121	SYLPTNTVETLRVSGANMILLRSRGDILLVYLLAHCALYLLVPPSPCAVQVCGSPYQYCA	180	
DB	121	SYLPTNTVETLRVSGANMILLRSRGDILLVYLLAHCALYLLVPPSPCAVQVCGSPYQYCA	180	

XX AAY26580;
AC 13-SEP-1999 (first entry)
XX Human telomerase reverse transcriptase (hTERT) enzyme.
XX Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication; human.
XX Homo sapiens.
XX WO9927113-A1.
XX 03-JUN-1999.
XX 25-NOV-1998; 98WO-US025211.
XX 26-NOV-1997; 97US-00979742.
XX 16-MAR-1998; 98US-00042460.
XX (GERO-) GERON CORP.
XX (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX Morin GB, Allsopp R, Depinho R, Greenberg R;
XX WPI; 1999-347722/29.
XX Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
PT nucleic acids.
XX Disclosure; Fig 3; 135pp; English.
XX The invention relates to a mouse telomerase reverse transcriptase (mTERT)
CC assays. Compositions containing mTERT can be used in telomere length
CC assays. Isolated mTERT is useful as an immunogen for the production of
CC monoclonal or polyclonal antibodies. The method is useful for assessing
CC the degree of purification and identification of new mTERT species, such
CC as an mTERT allele, homolog or isoform, or to screen for modulators
CC (antagonists and agonists) of telomerase-mediated DNA replication.
CC Antagonists and agonists of mTERT can be used to modify the activity of
CC other telomerase enzymes such as human TERT (hTERT). The present sequence
CC represents a human TERT enzyme
XX Sequence 1132 AA;
Query Match 59.4%; Score 3505; DB 2; Length 1132;
Best Local Similarity 62.4%; Pred. No. 0;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;
Qy 1 MTRAPRCNVRSLRSRYREWFVPLATFVRLGPEGRRLVQGDPKIYRTLVACQCLVCMHW 60
Db 1 MPRAPRCNVRSLRSRYREWFVPLATFVRLGPEGRRLVQGDPKIYRTLVACQCLVCPW 60
Qy 61 GSQPPADLSHFVSSLSKELVARVQRCERNERNVLAFGPELLNEARGGPPMAFTSSVR 120
Db 61 DARPPPAAPSRFQVSCLELVARVQRCERNERNVLAFGPELLNEARGGPPMAFTSSVR 120
Qy 121 SYLPNTVTETLRVSGAMLLLSRVGDDLLVLLAHALCALYLLVPPSCAYQVCGSPLYQICA 180
Db 121 SYLPNTVTDALRGSGAWGLLRLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGSPPLYQLGA 180
Qy 181 TTDIHWPSVSAVRPRTPVGRNFTNRLFLOQTKSSSRQBAKPLALPSRGTKRHLSLSTS 240
Db 181 ATQARPPPHAS-GPRRLG-----CERAWNHSVREAGVPLGLPAPGARRGGASRS 231
Qy 241 VPSAKKACYPVPRVEGP-----HRQVLPTEGKSM-VPSPARSEVPTAEKDLSSK 292
Db 232 LPLPKRPRRGAPEPRTVVGSGSWAHFGRTGSDRGFCVVSPAR-----PAEATSL 286
Qy 293 GKVSLSLS-GSVCCCHKPSTLSLSPRONAFQLRP-FIETRHFLYGRGDQERLNPSF 350
Db 287 GALSCTRSHSFVSGRHHAGPSTSRPRPMDTPCPVVAETKHFLYSSGD-KEQLRPSF 345

Qy 351 LLSNLPNLTGARRLVEIIFLGSRRPTSGPLCKRHLSSRYQWRPLFOQLLVNHAECQY 410
Db 346 LLSLSRPSLTGARRLVETIFLGSRRPMPGTGPRPLPRLPQRYQWRPLFLELLGNHACPY 405
Qy 411 VRLRSHCRFRANQOQVTDAL-----NTSPPHLMDLLRLHSSPQVY 452
Db 406 GVLLKTHCPLRAA---VTPAAGVCAREKPOGSVAAPEDDTDRRLVQLLRHSSPQVY 462
Qy 453 GFLRACLCKVVSASLWGRHNRPPKQLKFKSLGKYGKLSLOELMKMKVSDCHWLS 512
Db 463 GFVRACLRRLVPEGLWGRHNRFLRNTKFKSLGKHAKLSLOELTKWNSVDRCAWLR 522
Qy 513 SPGRDVRPAEHRRLRILATFLWLDVTYVOLLRSFFYITESTFQKRLFFYKSVWS 572
Db 523 SPGVGCVPAEHRRLREILAKFLHLMVSVVVELLSFFYVTTTQKRLFFYKSVWS 582
Qy 573 KLOSIGVROHLERVLRELSQSEVRHQDTWMLAMPICRLRPIKPNGLRPIVMSVMGT 632
Db 583 KLOSIGIRQHLKRVQLRELSAEVRQREARPAALLTSRLRPIKPDGLRPIVMDYVGA 642
Qy 633 RALGRKQAOHPTORLKTFLPSMLNYERTKPHLMGSSVLGMNDIYRTWRAFVLVRALDQ 692
Db 643 RTRERKRAERLTSRVKALFSLVNYERARRPGLLGASVLGDDIHRARWTFVLVRQAQDP 702
Qy 693 TPRMYFVKADVTGAYDAIPQGLVVEVANNIRSESTYCIROYAVVRDQSGQVHKSFR 752
Db 703 PPSELYFVKDVTGAYDTIPQDLTEVIASIIK-PQNTYCVRYAVVQKAAHGVKAFKS 761
Qy 753 QVTTLSDLPYMQQFLKHLQSDASALRNSVIEQSISSMNESSSLPDPFFLHFLRHGVK 812
Db 762 HVSTLTDLPYMRQFVAHLQET--SPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVR 819
Qy 813 IGRCYTCOGIIPQSSSLTLLCSLCFQDMENKLEAEVORDGLLRFPVDDFLVTPHLQ 872
Db 820 IRGKSYVQCQIPQSGSLTLLCSLCYGDMEKLFAGIRDRGLLRLLVDDFLVTPHLTH 879
Qy 873 AKTFLSLTVHGVPEYGCMLNKTQVNVFPVEPGTLLGGAAPYQLPAHCLFPWCGLLDTQT 932
Db 880 AKTFLRLVRGVEYGCVMNLKTVNVFPVEDEALGCTAFVQMPAHGLFPWCGLLDTRT 939
Qy 933 LEVFCDSYGAQTSIKTSLTFQSVFKAGKTMWNKLSVLRLKCHGLFLDLQVNSLQTVCI 992
Db 940 LEVQSDYSYARTSIRASLTFRNGFKAGRNRRKLFGLVRLKCHSLFDLQVNSLQTVCT 999
Qy 993 NIYKIFLLOAVRPHACVQLPDPORVRKNTLTFGLIISSOASCCYAILKVNPGMTLKAS 1052
Db 1000 NIYKILLLOAVRPHACVQLPDPORVRKNTLTFGLIISDTASLCYSLKAKNAGMSLGAK 1059
Qy 1053 GS---PPEAAHMLCYQAFLLKLAHSHVIYKCLLGLPRLTAQKLCRKLPEATMTILKAAA 1109
Db 1060 GAAGPLPSEAVQMLCHQAFLLKLTNRHTVYVPLLSGLRTAQTQLSRKLPGTTLTALBAAA 1119
Qy 1110 DPALSTDPQTILD 1122
Db 1120 NPALPSDFKTILD 1132
RESULT 13
AAG64859
ID AAG64859 standard; protein; 1132 AA.
XX AAG64859;
AC AAG64859;
XX 21-SEP-2001 (first entry)
DT Heart muscle cell differentiation related protein SEQ ID NO: 31.
DB Heart muscle cell; human; cell differentiation; heart disease.
XX Homo sapiens.
XX WO200148151-A1.
XX

XX PD 05-JUL-2001.
XX PF 27-DEC-2000; 2000WO-JP009323.
XX PR 28-DEC-1999; 99JP-00372826.
XX PR 28-FEB-2000; 2000WO-JP001148.
XX PR 02-NOV-2000; 2000WO-JP007741.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
PI Yamada Y;
XX DR WPI; 2001-425656/45.
XX DR N-PSDB; AAH48235.
XX PT Cells capable of differentiating into cardiomyocytes and originating in
PT bone marrow or umbilical blood cells for study of cardiomyocyte
PT differentiation and treatment of heart disease.
XX PS Claim 87; Page 143-147; 183pp; Japanese.
XX CC The present invention provides cells originating in the human bone marrow
CC or umbilical blood cells which are capable of differentiating into
CC cardiomyocytes. These cells are useful in the treatment of diseases
CC involving heart muscle degeneration, such as myocardial infarction, and
CC the study of cardiomyocyte differentiation. The present sequence is a
CC protein described in the exemplification of the invention
XX SQ Sequence 1132 AA;
Query Match 59.4%; Score 3505; DB 4; Length 1132;
Best Local Similarity 62.4%; Pred. No. 0;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;
QY 1 MTRAPRCAPVRSLLRSRYEVWPLATFVRRLLGPEGRLVQPGDKIYRTLVAQCLVCMHW 60
DB 1 MPRAPCRAVRSLLRSRYEVWPLATFVRRLLGPEGRLVQPGDKIYRTLVAQCLVCPW 60
QY 61 GSQPPADLSFHOVSLKELVARVQRLCERNERNVLPAGFELLNEARGGPPMATSSVR 120
DB 61 DARPPPAAPSPFRQVSLKELVARVQRLCERGAQNVLPAGFALLDARGGPPAFTTSVR 120
QY 121 SYLPTNTVTLTAVSGAWMLLSRGDGLVLLAHCALVLLVPPSCAYQVCGSPLYQICA 180
DB 121 SYLPTNTVTLTAVSGAWMLLSRGDGLVLLAHCALVLLVPPSCAYQVCGSPLYQLGA 180
QY 181 TTDIWPVSASYPTRPVGRNFTNLRLQOIKSSSRQEAPEKPLALPSRGTKEHLSLTSTS 240
DB 181 ATQARPPPHAS-GPRRLG-----CERANHSVREAGVFLGLPAPGARRGGASRS 231
QY 241 VPSAKKARCYVPVRVEGP-----HROVLTPSGKSW-VSPARSPEVPTAEKDLSSK 292
DB 232 LPLKPRPRGAAPPEPTPVGQSWAHFGRTRGSPDRGFCVVSPAR-----PAEATSLE 286
QY 293 GKVSIDLSL-GSVCKKHPSSTLSLPPRQNAQLRP-PIETRFLYSRGQDQRLNPSF 350
DB 287 GALSUTRSHPSVGQHHAGPPSTRPRPMDTPCPVVAETKFLYSSG-KEQLRPSF 345
QY 351 LLSNLQPNLTGARRLVEIIFLGSRRPTSQFLCRLHLSRRYQMRPLFQQLLVNHAQCQ 410
DB 346 LLSLSRPSLTGARRLVETIFLGSRRPMTGTPRLPRLPQRYQMRPLFLELGNHAQCQ 405
QY 411 VLLRSHCRFTANQOVTAL-----NTSPPHMLDLHSSFWQVY 452
DB 406 GYLLKTHCPLEAA---VTPAAGVCAREKPGQSVAAPEBEDTDPRLVLQLLRHQSSFWQVY 462
QY 453 GFLRACLCKVVSASLWGTTHNERRFFKNLKKFISLGYCKLSLOELMWMKVEDCHMLRS 512
DB 463 GFLRACLRLRVLPPGLGSHNRRFLNRTKFIISLGHAKUSLQELTWKMSVRDCAWLRR 522
QY 513 SPGKDRVPAAEHRLRERILATFLFWMMDTYVQLLRSFFYITESTFQKNRLLFFYRKSVMS 572

DB 523 SPGVGCVPAAEHRLRERILAKFLHLMSSVYVVELLSPPYVVTETTFQKNRLLFFYRKSVMS 582
QY 573 KLSIGVROHLERVELRELSEQEVVHODTWLAMPICRLRETPKNGNLRPIVNMVSVMGT 632
DB 583 KLSIGIRQHLKRVQLRELSEAEVQHREARPALLTSLRFLPKPDGLRPIVNMDDYVUGA 642
QY 633 RALGRKQAOHFTQRLKTLFSLMYERTKPHLMGSSVLGMNDIYRTWRAPFLVRALDQ 692
DB 643 RTFREKRAERLTSRVKALFSLVNERARRPCLLGASVLGLDDIHRAWRTFVLVRADQP 702
QY 693 TPRMTFVKADVTGAYDAIPQKLVVVVANMIRHSESTYCIROYAVVRDSDQOVHKSFR 752
DB 703 PPELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PONTYCVRYAVVQKAAHGHVRKAPKS 761
QY 753 QVTTLSLQPYMGQFLKHLQSDASALRNSVVIEOSISNMESSLSLDFPLHPLRHSVVK 812
DB 762 HVTSLTDLQPYMRQVAHLQET--SPLKDAVVIEQSSLSNEASSGLFDVFLRFMCHHAVR 819
QY 813 IGDRCYTCQGIPOGSSLSLTLCSLCFGDMENKLPARYQRDGLLRVDDFLVTPHLDQ 872
DB 820 IRGKSYVQCQGIPOGSSLSLTLCSLCYGDMMENKLPAGIRRDGLLRVDDFLVTPHLDQ 879
QY 873 AKTFSLTVHGVPEYGCINLQKTVVNPFPBPTLGGAAPYQLPAHCLFPWCGLLLDTQT 932
DB 880 AKTFSLTVHGVPEYGCINLQKTVVNPFPBPTLGGAAPYQLPAHCLFPWCGLLLDTQT 939
QY 933 LEVFCDSYGAQTSIKTSLTQSVPKACKTWKLLSVLRKCKHCLFLDLQVNSLQTVCI 992
DB 940 LEVQSDSYARTSIRASLTFRNGPKAGNRMRRLFGVLRKCKHCLFLDLQVNSLQTVCI 999
QY 993 NIYKIFLQAYRFHACVQLPFDQVRVKNLTPFLGIISSQASCCYAILKVNKPMGMTLKAS 1052
DB 1000 NIYKILLQAYRFHACVQLPFDQVRVKNLTPFLGIISSQASCCYAILKVNKPMGMTLKAS 1059
QY 1053 GS---FPPEAAHWLCYQAPFLKLAHSAHVIYKCLLGPLTAQKLCRKLPEATMTILKAAA 1109
DB 1060 GAAGPLPSEAVQWLCHQAPFLKLTFRHRYVTVYVPLLSGLRTAQQLSRKLPGLTTLTALEAAA 1119
QY 1110 DPALSTDFTILD 1122
DB 1120 NPALSPDFKTLID 1132
RESULT 14
AAG64329
ID AAG64329 standard; protein; 1132 AA.
XX AAG64329;
XX AC
XX DT 24-SEP-2001 (first entry)
XX Human protein #2.
DE Angiogenesis; cardiact; cell differentiating agent; bone marrow;
KW heart muscle cell; heart disease; human.
XX Homo sapiens.
XX WO200148149-A1.
XX PD 05-JUL-2001.
XX PF 28-FEB-2000; 2000WO-JP001148.
XX PR 28-DEC-1999; 99JP-00372826.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;
XX DR WPI; 2001-418252/44.
DR N-PSDB; AAH49601.

XX New adult bone marrow-originated cells capable of differentiating into
PT heart muscle cells, applicable as remedies for various heart diseases
PT particularly with damaged heart muscle accompanying degeneration.
XX
PS Disclosure; Page 128-134; 158pp; Japanese.
XX
CC The present invention relates to cells isolated from bone marrow, which
CC are capable of at least differentiating into heart muscle cells. The
CC cells are applicable as remedies for various heart diseases particularly
CC with damaged heart muscle accompanying degeneration. The present sequence
CC was used to illustrate the present invention
XX
SQ Sequence 1132 AA;

Query Match 59.4%; Score 3505; DB 4; Length 1132;
Best Local Similarity 62.4%; Pred. No. 0;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;
Qy 1 MTRAPRCAPVRLSRLSRVREYVPLATFVRRILGPGRRRLVQPDPKIVHTLVAQCILCMHW 60
Db 1 MPRAPRCARSLRLSRHTREYVPLATFVRRILGPGRRRLVQPDPAAFALVAQCILCVPW 60
Qy 61 GSQPPADLSFHQVSSSLKELVARVQRLCERNERNVLAFFGELLNEARGSPMAFTSSVR 120
Db 61 DARPPAPAPSPQVSLKELVARVQLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
Qy 121 SYLNTVJETLRVSGANWMLLSRVGDDLLVLLAHALYLLVPPSCAYQVCGSPYQICA 180
Db 121 SYLNTVTDALRGSGAMGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 TTDIWPVSASVRLTRPVGRFTNLRLFLQIKSSSRQEAAPKPLALPSRGTGRHLSLSTS 240
Db 181 ATQARPPPHAS-GPRRRUG-----CERANWHSVREAGVPLGLPAPGARRRGGSASRS 231
Qy 241 VPSAKKARCVPRVVEEGP-----HRQVLFTSGKSW-VPSPARSEVPTABKLSKK 292
Db 232 LPLPKRPRGAAPERPTVQGGSWAHGPRTRGSDRGFCVSPAR-----PAEANTSL 286
Qy 293 GKVDLSLS-GSVCCCHKPSSTLSLPPRONAQLRP-FIETRIPLYSRGQGRNLNPSF 350
Db 287 GALSCTRHSHPVGRQHAGPSTSRPPRWDTPCPVYAEYTGFLYSSGD-KEQLRPSF 345
Qy 351 LLSNLQPNLTGARRLVEITFLGSRPRTSGPLCRTHLSRRYQWMPPLFOQLLVNHAECQY 410
Db 346 LLSLRPSLTGARRLVEITFLGSRPRTSGPLCRTHLSRRYQWMPPLFOQLLVNHAECQY 405
Qy 411 VRLLRSHCRFTANQQVTDAL-----NTSPHMLDLRLHSPWQVY 452
Db 406 GVLLKTHCPRLAA---VTPAAGVCAREKPGQSVAAPEBEDTDRRLVQLLRQHSSPWQVY 462
Qy 453 GFLRACLCKVYSASLWGRTHRRNRRPFLKXFLSLGKYGKLSLOELMWKMKVEDCHWLS 512
Db 463 GFVRACLRLVPPGLWGRSHRRNRRFLRNTKXFLSLGKAKLSLOELTWKMSVRDCAMLR 522
Qy 513 SPKDRVPAAEHLRERLILATFLWMDTYVQVLLRSFFYITESTFOKNRLFYFRKSVWS 572
Db 523 SPGVGCVPAAEHRLRERLILATFLWMDTYVQVLLRSFFYITESTFOKNRLFYFRKSVWS 582
Qy 573 KLOSGIVRQHILRVLRLSLOEVRHHODTWLAMPICRLRIPKPNGLRPIVNNMSYSGT 632
Db 593 KLOSGIGIRHQLKRVQLRSEAEVRQREARPALTSRLRIPKPDGLRPIVNNMDYVGA 642
Qy 633 RALGRKQAQHTQRLKTLFPMNLNRYTKHPHLMGSSVLGNDIYRTWRATFLVRALDQ 692
Db 643 RTFREKRAERLTSRKALFSLNTERARRPCLLGASVLGLDDIHRAWRTFLVRADQP 702
Qy 693 TPRMYFVKADVTGADAIPOGKLVENVANMRHSESTYCIROYAVVRDSDGQVHKSPRR 752
Db 703 PPELYFVKVDVTGADYITPDQRLTEVIAIILK-PONTYCVRYAVVQAAHGHVRKAPKS 761
Qy 753 QVTTLSDLQPYMGQPLKHLQSDASALRNSVVIEQISIMNBSSSSLFFFLHFLRHSYVK 812

Db 762 HVSTLTDLQPMYRQFVAHLQET--SPLRDVAVVIEQSSSLNEASSGLFDVFLRFMCHHAVR 819
Qy 813 IGDRCTYQCCGIGIQQSSSLTLLCSLCFQDMENKLFQVQDRDGLLRFFVDDPLLVTPHLQ 872
Db 820 IRGKSYVQCCGIGIQQSSSLTLLCSLCYQDMENKLFAGIRDRDGLLRVDDPLLVTPHLTH 879
Qy 873 AKTFPLSLVHGVPEYGCWMLNLOKTVVNFPPVPGTLGGAAPYQLPAHCLFPMCGLLLDQT 932
Db 880 AKTFPLRLVHGVPEYGCWMLNLOKTVVNFVDEALGGTAFQMPAHGLFPMCGLLLDTRT 939
Qy 933 LEVFCDSYGAQTSIKTSITFSQSVFKAGKTWRNKLKSLVRLKCHGLFLDLQVNSLQTVCI 992
Db 940 LEVQSDYSYARTSIRASLTFRNGFKAGRNRRKLFGLVRLKCHSLFLDLQVNSLQTVCT 999
Qy 993 NIYKIFLLQAYRFHACVQLPQDQVRKNTLTFGLIISSOASCCYAILKVNPNQMTLKAS 1052
Db 1000 NIYKILLQAYRFHACVQLPQDQVRKNTLTFGLIISSOASCCYAILKVNPNQMTLKAS 1059
Qy 1053 GS---FPPEAAHMLCYQAFLLKLAHSAVYIKLLGLPLRTAQKLCRKLPEATMTILKAAA 1109
Db 1060 GAAGPLPSEAVQMLCHQAFLLKLTTRHRTVTVPLIGSLRTAQTLQSRKLPGLTTLTALEAAA 1119
Qy 1110 DPALSTDFQITLD 1122
Db 1120 NPALPSDFKTILD 1132
RESULT 15
AAB99930
ID AAB99930 standard; protein; 1132 AA.
XX AC AAB99930;
XX DX 26-SEP-2001 (first entry)
XX Human telomerase protein sequence SEQ ID NO:31.
XX DE Differentiation; heart muscle cell; cytokine; transcription factor;
XX KW proliferation; surface antigen; heart disease; cardiomyocyte;
XX KW bone marrow; umbilical blood cell; heart muscle degeneration;
XX KW myocardial infarction.
XX OS Homo sapiens.
XX XX WO200148150-A1.
XX XX 05-JUL-2001.
XX XX 02-NOV-2000; 2000WO-JP007741.
XX XX 28-DEC-1999; 99JP-00372826.
XX XX 28-FEB-2000; 2000WO-JP001148.
XX XX (KYOW) KYOWA HAKKO KOGYO KK.
XX XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
XX XX Yamada Y;
XX XX WPI; 2001-425655/45.
XX XX N-PSDB; AAH44366.
XX XX Cells capable of differentiating into cardiomyocytes and originating in
XX XX bone marrow or umbilical blood cells for study of cardiomyocyte
XX XX differentiation and treatment of heart disease.
XX XX Claim 146; Page 137-141; 187pp; Japanese.
XX XX The present invention describes cells originating in bone marrow or
XX XX umbilical blood cells which are capable of differentiating into
XX XX cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
XX XX differentiation of the cells; (2) a method for carrying out the
XX XX differentiation into cardiomyocytes, regulated by a promotional and/or
XX XX inhibitory factor; (3) a method for the differentiation of the cells into

cell types other than cardiomyocytes; (4) drug compositions promoting the formation of heart muscle and regeneration of heart tissue which contain the cells; (5) a method for the production of antibodies which recognise the cells, especially antibodies which recognise a surface antigen on the cells; (6) a method for screening factors which promote the proliferation of the cells; (7) a method for immortalising the cells by expressing telomerase in them; (8) drug compositions for the treatment of heart disease which contain the immortalised cells; and (9) cell-free supernatant from the culture of the cells and its use in promoting their differentiation into cardiomyocytes. The cells are used in the treatment of diseases involving heart muscle degeneration, such as myocardial infarction and in the study of cardiomyocyte differentiation. AAH44351 to AAH44409 and AAB99915 to AAB99935 represent sequences used in the exemplification of the present invention

Sequence 1132 AA;

Query Match	59.4%;	Score	3505;	DB	4;	Length	1132;
Best Local Similarity	62.4%;	Pred.	No. 0;				
Matches	719;	Conservative	122;	Mismatches	260;	Indels	52;
Gaps	13;						
C	1	MTRAPRCAPVRSLLSRVREVMPLATFVRRLGPEGRLVQPGDPKIRYRTLVQAQCLVCMHW	60				
Q	1	MPRAPRCAPVRSLLSRVREVMPLATFVRRLGPEGRLVQPGDPKIRYRTLVQAQCLVCMHW	60				
C	61	GSQPPADLSFHQVSSKLKELVARVQRLCERNERNVLAFFGELLNEARGPPMAFTSSVR	120				
Q	61	DARPPAPAPSFQVQCKELKELVARVQRLCERNERNVLAFFGELLNEARGPPMAFTSSVR	120				
C	121	SYPNTVITLAVSGAMLLSRVGDLLVYLAHICALYLLVPPSCAYOVCSPLYQCA	180				
Q	121	SYPNTVITDALRGSGAWGLLRVGDVLLVLAHICALYLLVPPSCAYOVCSPLYQCA	180				
C	181	TTDIAPSVSAYRTPRPGRNFTNLRFLOQIKSSRQEAPEKPLAPSRGCTKREHLSITSTS	240				
Q	181	ATQARPPPHAS-GPRRLG-----CERAWNHSVREAGVFLGAPGARRRGGASRS	231				
C	241	VPSAKKARCPVPRVEEGP-----HRQVLTTPSGKSW-VPSPARSPVPTAEKDLSSK	292				
Q	232	LPLPKRPRGAPEPERTVPGQSWAHPGRTGRGSDRGFCVVSAPAR-----PAERATSLE	286				
C	293	GKVSLSLS-GVCKCHKPSSLSLSPRONAFQLRP-FIETRHFLYSRGDQERLNPSF	350				
Q	287	GALSGRTRSHPSVGRQHAGPSPSTRPRPMDTPCPVPVYAEKFLYSSGD-KEQLRPSF	345				
C	351	LLSNLQPNLTGARRIVEIIFLGRSPTSGPLCKTRHLSRYWQMRPLFOQLLVNHAECOY	410				
Q	346	LUSSLRPSLTGARRIVETIFLGRSPMPTPRRLPRLPQRYWQMRPLFLELIGNHAQCPY	405				
C	411	VLLRSHCRFTANQOVTDAL-----NTSPPHLMDLLRLHSSPWQVY	452				
Q	406	GVLKXTHCPLRAA---VTPAAGVCAREKPGQSVAAPEBEDTDPRLVQLLRQHSPPWQVY	462				
C	453	GFLRACLCKVVSASLWGTTHNRRRFPKNTKKFISLGKYKLSLOELMMWOKVEDCHWLS	512				
Q	463	GFVRACLRRLVPPGLWGRSHNRRFLNKKFISLGKHAQKLSLOELTWKMSVRDCAWLRR	522				
C	513	SPGKRVPAAEHRLRERILLATFLWMDTVVQLLRSPEYITESTFQKRLFFYRKSVMS	572				
Q	523	SPGVGCVPAAEHRLRERILLATFLWMDTVVQLLRSPEYITESTFQKRLFFYRKSVMS	582				
C	573	KLQSIGVRQHLRRLRRELSQBEVRHQDTWLMPICLRIFPKPNGLRPIVNMYSMGT	632				
Q	583	KLQSIGIRQLKRVQLRELSAEVROHREARPALITSLRFLFKPDGLRPIVNDYVGA	642				
C	633	RALGRKQAOHTQRTKTLFSLMNYERTKPHLMGSSVLGMDIYRTWPAFVLRVALDQ	692				
Q	643	RTFRREKRAERLTSRKALFSLVNYERARRPGLLGASVLGLDIIHRAWRTFVLRVAQDP	702				
C	693	TPRMFYKADVTGAYDAIPQGLKVEVWAMIRHSESTYCIROYAVVRDSQGVHKSFR	752				
Q	703	PELYFVKVDVTGAYDTIPQDRLTEVIASIIK-PONTYCVRRYAVVQKAAHGHVRKAFKS	761				

Search completed: May 15, 2006, 13:30:22
Job time : 196 secs

QY	753	QVTLSDLPYMGQFLKHLQSDASALRNSVUIEQSISWNESSSLPDPFLPLRHSVVK	812
DB	762	HVSTLTDLPYMRQFVAHLOET--SPLRDVUIEQSSSLNEASSGLFDVFLRPMCHAVR	819
QY	813	IGDRCYTCOCQIPQSSSLTLLCSLCFGDMENKLPABYQORDGLLRFRVDDFLLVTPHLDQ	872
DB	820	IRGKSYVOCQIPQSSILSTLLCSLCYGDMMENKLPAGIRRDGLLRVDDFLLVTPHLDQ	879
QY	873	AKTFLSTLVHGVPEYGCMMINIKTVNPPVBPFTLGGAAAPYQLPAHCLFPPWGLLLDTQT	932
DB	880	AKTFLRTLVRGVPEYGCMMINIKTVNPPVBPFTLGGAAAPYQLPAHCLFPPWGLLLDTQT	939
QY	933	LEVPCDYSYAGTSIKTSITQSVPFKAGKTWRNKLLSVLRKCHGLFLDLQVNSLOTVCI	992
DB	940	LEVQSDYSYARTSIRASLTFRNPGFAGNRKRKLFGVLRKCHSLFLDLQVNSLOTVCT	999
QY	993	NIYKIFLLQAYRFHACVQLPDPDORVRKNLTPFLGIISSQASCCYAILKVNKPMGMLKAS	1052
DB	1000	NIYKILLQATRFHACVQLPDPDORVRKNLTPFLGIISSQASCCYAILKVNKPMGMLKAS	1059
QY	1053	GS---PPPEAAHWLCYQAFLLKLAHSAHSVIYKCLLGLPLRTAQKLLCRKLPEATMTILKAA	1109
DB	1060	GAAGPLPSEAVQWLCHQAFLLKLTERRVTVYVPLIGSLRTAQQLSRKLPGLTTLTALEAAA	1119
QY	1110	DPALSTDPQTILD	1122
DB	1120	NPALPSDFKTILD	1132

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